

86136

SEARCH REQUEST FORM

Access DB#

23

Scientific and Technical Information Center

CRFE

Requester's Full Name: Lisa V. Cook Examiner #: 77134 Date: 2/5/03
 Art Unit: 1641 Phone Number 305-0808 Serial Number: 09/845,729
 Mail Box and Bldg/Room Location: CM1-7E12 Results Format Preferred (circle): PAPER DISK E-MAIL
 Office CM1 7B-17

If more than one search is submitted, please prioritize searches in order of need:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Biopolymer marker indicative of disease state having a molecular weight of 1350 daltons
 Inventors (please provide full names): George Jackowski, Brad Thatcher, John Marshall, Tammy Vrees

Earliest Priority Filing Date: 4/30/01

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Sequence Search for: SESNF LAE GGGVR
Seq. Id. No. 1

Sequence utility in detecting myocardial infarction or renal failure. Biopolymer marker/antibodies assay.

also see attached claims + bib sheet

Thanks, ☺
 L/Cook

RECEIVED

FEB -6 2003

STIC

sig 1 AA @ 13

Point of Contact:
 Beverly Shears
 Technical Info. Specialist
 CM1 1E05 Tel: 308-4994

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: Beverly e 4994 NA-Sequence (#) STN ✓
 Searcher Phone #: _____ AA Sequence (#) _____ Dialog _____
 Searcher Location: _____ Structure (#) _____ Questel/Orbit _____
 Date Searcher Picked Up: _____ Bibliographic _____ Dr. Link _____
 Date Completed: 02-11-03 Litigation _____ Lexis/Nexis _____
 Searcher Prep & Review Time: 3 Fulltext _____ Sequence Systems _____
 Technical Prep Time: _____ Patent Family _____ WWW/Internet _____
 Online Time: 21 Other _____ Other (specify) CGN

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Cook, L.
09/845729

09/845729

FILE "REGISTRY" ENTERED AT 09:18:47 ON 11 FEB 2003
L1 2 S SESDFLAEGGGVR/SQSP

L1 ANSWER 1 OF 2 REGISTRY COPYRIGHT 2003 ACS
RN 474451-10-0 REGISTRY
CN Glycine, L-.alpha.-aspartyl-L-seryl-L-.alpha.-glutamyl-L-seryl-L-
.alpha.-aspartyl-L-phenylalanyl-L-leucyl-L-alanyl-L-.alpha.-
glutamylglycylglycylglycyl-L-valyl-L-arginyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 7: PN: US20020160420 PAGE: 12 unclaimed sequence
SQL 15

SEQ 1 DSESDFLAEG GGVRG
=====

HITS AT: 2-14

REFERENCE 1: 137:348834

L1 ANSWER 2 OF 2 REGISTRY COPYRIGHT 2003 ACS
RN 473552-35-1 REGISTRY
CN L-Arginine, L-seryl-L-.alpha.-glutamyl-L-seryl-L-.alpha.-aspartyl-L-
phenylalanyl-L-leucyl-L-alanyl-L-.alpha.-glutamylglycylglycylglycyl-
L-valyl- (9CI) (CA INDEX NAME)
SQL 13

SEQ 1 SESDFLAEGG GVR
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HITS AT: 1-13

REFERENCE 1: 137:334901

FILE "HCAPLUS" ENTERED AT 09:19:16 ON 11 FEB 2003
L2 2 S L1

L2 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:833425 HCAPLUS
DOCUMENT NUMBER: 137:334901
TITLE: Alpha fibrinogen biopolymer marker indicative of
myocardial infarction or renal failure having a
molecular weight of 1350 daltons
INVENTOR(S): Jackowski, George; Thatcher, Brad; Marshall,
John; Yantha, Jason; Vrees, Tammy
PATENT ASSIGNEE(S): Can.
SOURCE: U.S. Pat. Appl. Publ., 10 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002160528	A1	20021031	US 2001-845729	20010430
WO 2002088722	A2	20021107	WO 2002-CA610	20020426
WO 2002088722	A3	20021227		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH,
CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD,
GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,

Searcher : Shears 308-4994

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09/845729

LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,
TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ,
BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,
CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT,
SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,
SN, TD, TG

PRIORITY APPLN. INFO.:

US 2001-845729 A 20010430

AB The instant invention involves the use of a combination of preparatory steps in conjunction with mass spectroscopy and time-of-flight detection procedures to maximize the diversity of biopolymers which are verifiable within a particular sample. The cohort of biopolymers verified within such a sample is then viewed with ref. to their ability to evidence at least one particular disease state; thereby enabling a diagnostician to gain the ability to characterize either the presence or absence of said at least one disease state relative to recognition of the presence and/or the absence of said biopolymer. Serum samples were analyzed by SELDI-TOF using the Ciphergen PROTEINCHIP system and the disease specific marker identified by the sequence SESDFLAEGGGVR and characterized as a .alpha. fibrinogen having a mol. wt. of 1350 daltons was found. This marker is indicative of myocardial infarction or renal failure.

IT 473552-35-1

RL: ANT (Analyte); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(alpha fibrinogen biopolymer marker of 1350 daltons indicative of myocardial infarction or renal failure)

L2 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:833395 HCAPLUS

DOCUMENT NUMBER: 137:348834

TITLE: Process for diagnosis of physiological conditions by characterization of proteomic materials

INVENTOR(S): Jackowski, George; Thatcher, Brad; Marshall, John; Yantha, Jason; Vrees, Tammy

PATENT ASSIGNEE(S): Can.

SOURCE: U.S. Pat. Appl. Publ., 25 pp.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002160420	A1	20021031	US 2001-846330	20010430
WO 2002088744	A2	20021107	WO 2002-CA623	20020429

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

Searcher : Shears 308-4994

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09/845729

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE,
CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT,
SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,
SN, TD, TG

PRIORITY APPLN. INFO.:

US 2001-846330 A 20010430

AB The present invention discloses the use of proteomic investigation as a diagnostic tool; and particularly teaches the use of proteomic investigative techniques and methodol. to det. a proteomic basis for the development and progression of abnormal physiol. conditions and the development and characterization of risk assessment, diagnostic and therapeutic means and methodologies. Serum samples from patients suffering from a variety of diseases in Syndrome X were analyzed by SELDI mass spectrometry using the Ciphergen PROTEINCHIP system to discern disease markers.

IT **474451-10-0**

RL: PRP (Properties)

(unclaimed sequence; process for diagnosis of physiol. conditions by characterization of proteomic materials)

FILE 'HOME' ENTERED AT 09:19:25 ON 11 FEB 2003

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COOK, L.
09/845729
Seq. ID 1 w/
Interf

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2003, 16:00:57 ; Search time 354 Seconds
(without alignments)
23.677 Million cell updates/sec

Title: US-09-845-729-1
Perfect score: 65
Sequence: 1 SESDFLAEGGGVR 13

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main.*
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26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	87.7	12	22	US-09-845-725-1
2	57	87.7	15	22	US-09-845-719A-1
3	57	87.7	16	1	PCT-US99-03350A-25
4	57	87.7	16	8	US-08-469-141-56
5	57	87.7	16	12	US-08-844-462-14
6	57	87.7	16	14	US-09-025-319A-25

7	57	87.7	16	19	US-09-525-269-25	Sequence 25, Appl
8	57	87.7	16	20	US-09-622-561-25	Sequence 25, Appl
9	57	87.7	16	20	US-09-648-816-25	Sequence 25, Appl
10	57	87.7	16	20	US-09-648-816A-25	Sequence 25, Appl
11	57	87.7	16	20	US-09-648-816A-109	Sequence 109, Appl
12	57	87.7	16	20	US-09-648-816B-25	Sequence 25, Appl
13	57	87.7	16	20	US-09-857-276-1135	Sequence 1135, App
14	57	87.7	16	22	US-09-826-290-352	Sequence 352, App
15	57	87.7	16	22	US-09-845-765-1	Sequence 1, Appli
16	57	87.7	16	22	US-09-846-780-1	Sequence 1, Appli
17	57	87.7	17	1	PCT-US02-14741-10	Sequence 10, Appl
18	57	87.7	17	1	PCT-US02-22821-53	Sequence 53, Appl
19	57	87.7	17	8	US-08-469-141-46	Sequence 46, Appl
20	57	87.7	17	20	US-09-657-276-1136	Sequence 1136, App
21	57	87.7	17	25	US-10-142-935-10	Sequence 10, Appl
22	57	87.7	17	25	US-10-197-954-53	Sequence 53, Appl
23	57	87.7	18	8	US-08-469-141-55	Sequence 55, Appl
24	57	87.7	19	8	US-08-469-141-54	Sequence 54, Appl
25	57	87.7	20	1	PCT-US99-03350A-26	Sequence 26, Appl
26	57	87.7	20	8	US-08-469-141-53	Sequence 53, Appl
27	57	87.7	20	8	US-08-478-260-1	Sequence 1, Appli
28	57	87.7	20	8	US-08-480-126-1	Sequence 1, Appli
29	57	87.7	20	8	US-08-483-990-1	Sequence 1, Appli
30	57	87.7	20	14	US-09-025-319A-26	Sequence 26, Appl
31	57	87.7	20	19	US-09-525-269-26	Sequence 26, Appl
32	57	87.7	20	20	US-09-622-561-26	Sequence 26, Appl
33	57	87.7	20	20	US-09-648-816-26	Sequence 26, Appl
34	57	87.7	20	20	US-09-648-816A-26	Sequence 26, Appl
35	57	87.7	20	20	US-09-648-816A-110	Sequence 110, App
36	57	87.7	20	20	US-09-648-816B-26	Sequence 26, Appl
37	57	87.7	21	8	US-08-469-141-45	Sequence 45, Appl
38	57	87.7	22	8	US-08-469-141-44	Sequence 44, Appl
39	57	87.7	22	8	US-08-469-141-52	Sequence 52, Appl
40	57	87.7	25	21	US-09-757-774-16	Sequence 16, Appl
41	57	87.7	30	3	US-07-963-538-9	Sequence 9, Appli
42	57	87.7	30	14	US-09-086-664-9	Sequence 9, Appli
43	57	87.7	30	14	US-09-087-371-9	Sequence 9, Appli
44	57	87.7	44	27	US-60-160-203-3985	Sequence 3985, App
45	57	87.7	360	1	PCT-US00-05989-587	Sequence 587, App

ALIGNMENTS

RESULT 1
US-09-845-725-1
; Sequence 1, Application US/09845725
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; TITLE OF INVENTION: OF 1206 DALTONS
; FILE REFERENCE: 2132.028
; CURRENT APPLICATION NUMBER: US/09/845,725
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-725-1

Query Match 87.7% Score 57; DB 22; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0095;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 1 EGDFLAEGGGVR 12

RESULT 2
US-09-845-719A-1

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; Sequence 1, Application US/09845719A
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; TITLE OF INVENTION: OF 1465 DALTONS
; FILE REFERENCE: 2132.035
; CURRENT APPLICATION NUMBER: US/09/845,719A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-719A-1

Query Match      87.7%; Score 57; DB 22; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2  ESDFLAEGGGVR 13
Db  4  EGDFLAEGGGVR 15

RESULT 3
PCT-US99-03350A-25
; Sequence 25, Application PC/TUS9903350A
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: Antimicrobial Peptides And Derived Metapeptides
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FULWIDER PATTON LEE & UTECHT, LLP
; STREET: 10877 Wilshire Blvd., Tenth Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90024
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: Hewlett Packard
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/03350A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/025,319
; FILING DATE: February 18, 1998.
; ATTORNEY/AGENT INFORMATION:
; NAME: Drucker, I. Morley
; NAME: Parkhurst, David G.
; REGISTRATION NUMBER: 19,751
; REGISTRATION NUMBER: 29,422
; REFERENCE/DOCKET NUMBER: REI 50480
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 824-5555
; TELEFAX: (310) 824-9696
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; FRAGMENT TYPE: internal fragment
; FEATURE:
; NAME/KEY: CS-FBP"
; IDENTIFICATION METHOD: By experiment
; OTHER INFORMATION: Microbicidal activities,
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; OTHER INFORMATION: PMIC = -78.53; MW = 1806.90; number of charged amino acids:
PCT-US99-03350A-25

Query Match      87.7%; Score 57; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2  ESDFLAEGGGVR 13
Db  5  EGDFLAEGGGVR 16

RESULT 4
US-08-469-141-56
; Sequence 56, Application US/08469141
; GENERAL INFORMATION:
; APPLICANT: MUMFORD, RICHARD A.
; APPLICANT: DAVIES, D.F. PHILIP
; APPLICANT: DAHLGREN, MARY E.
; APPLICANT: BOGER, JOSHUA S.
; APPLICANT: HUMES, JOHN L.
; TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
; TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: DR. CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,141
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 17461IB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)-594-6734
; TELEFAX: (908)-594-4720
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-469-141-56

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Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2  ESDFLAEGGGVR 13
Db  5  EGDFLAEGGGVR 16

RESULT 5
US-08-844-462-14
; Sequence 14, Application US/08844462
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, DALE H.
```

APPLICANT: TARR, GEORGE E.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Patent Administrator - Testa, Hurwitz &
ADDRESSEE: Thibault
STREET: High Street Tower, 125 High Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,462
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/796,598
FILING DATE: 07-FEB-1997
APPLICATION NUMBER: US 08/446,055
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FLYNN Esq., Kerry A.
REGISTRATION NUMBER: 33,693
REFERENCE/DOCKET NUMBER: SYP-115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-844-462-14

Query Match 87.7%; Score 57; DB 12; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| |||||
Db 5 EGDFLAEGGGVR 16

RESULT 6
US-09-025-319A-25
Sequence 25, Application US/09025319A
GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: Antimicrobial Peptides And Derived Metapeptides
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FULWIDER PATTON LEE & UTECHT, LLP
STREET: 10877 Wilshire Blvd., Tenth Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90024
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: Hewlett Packard
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,319A

FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Drucker, I. Morley
NAME: Parkhurst, David G.
REGISTRATION NUMBER: 19,751
REGISTRATION NUMBER: 29,422
REFERENCE/DOCKET NUMBER: REI 44454
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 824-5555
TELEFAX: (310) 824-9696
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: internal fragment
FEATURE:
NAME/KEY: RP-FBPa
IDENTIFICATION METHOD: By experiment
OTHER INFORMATION: antimicrobial activities,
PMIC = -78.53; MW = 1806.90; number of charged
OTHER INFORMATION: amino acids: 5
US-09-025-319A-25

Query Match 87.7%; Score 57; DB 14; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| |||||
Db 5 EGDFLAEGGGVR 16

RESULT 7
US-09-525-269-25
Sequence 25, Application US/09525269
GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
APPLICANT: Shen, Alexander J.
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED
METAPEPTIDES
FILE REFERENCE: 66081.415D1
CURRENT APPLICATION NUMBER: US/09/525,269
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antimicrobial peptide designed in part upon
OTHER INFORMATION: antimicrobial domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits.
US-09-525-269-25

Query Match 87.7%; Score 57; DB 19; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| |||||
Db 5 EGDFLAEGGGVR 16

```
RESULT 8
US-09-622-561-25
; Sequence 25, Application US/09622561
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED
; FILE REFERENCE: 660081.415C1
; CURRENT APPLICATION NUMBER: US/09/622,561
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-622-561-25
Query Match      87.7%; Score 57; DB 20; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 9
US-09-648-816-25
; Sequence 25, Application US/09648816
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED METAPEPTIDES
; FILE REFERENCE: 660081.415C1
; CURRENT APPLICATION NUMBER: US/09/648,816
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 2000-08-18
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/025,319
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: fragment or analogue of PMP-1 or PMP-2
US-09-648-816-25
Query Match      87.7%; Score 57; DB 20; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 10
US-09-648-816A-25
; Sequence 25, Application US/09648816A
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
```

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; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED
; FILE REFERENCE: 660081.415C1
; CURRENT APPLICATION NUMBER: US/09/648,816A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 09/622,561
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-648-816A-25
Query Match      87.7%; Score 57; DB 20; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 11
US-09-648-816A-109
; Sequence 109, Application US/09648816A
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED
; FILE REFERENCE: 660081.415C1
; CURRENT APPLICATION NUMBER: US/09/648,816A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 09/622,561
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antimicrobial peptide designed in part upon
; OTHER INFORMATION: microbiocidal domains from platelet microbial
; OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-648-816A-109
Query Match      87.7%; Score 57; DB 20; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 12
US-09-648-816B-25
; Sequence 25, Application US/09648816B
; GENERAL INFORMATION:
; APPLICANT: Yeaman, Michael R.
; APPLICANT: Shen, Alexander J.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND DERIVED
; FILE REFERENCE: 660081.415C1
; CURRENT APPLICATION NUMBER: US/09/648,816B
```

APPLICANT: Friedmann, David L.
APPLICANT: Herath, Herath Mudivanselage Athula Chandrasiri

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 10, 2003, 16:01:12 ; Search time 61 Seconds
(without alignments)
17.726 Million cell updates/sec

Title: US-09-845-729-1

Perfect score: 65

Sequence: 1 SESDFLAGGGVR 13

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 420310 seqs, 83175323 residues

Total number of hits satisfying chosen parameters: 420310

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:*

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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	100.0	13	5	US-09-845-729-1
2	57	87.7	16	6	US-10-325-162-1
3	57	87.7	70	5	US-09-724-676A-71849
4	57	87.7	70	5	US-09-724-676A-71849
5	57	87.7	93	5	US-09-724-676A-71847
6	57	87.7	93	5	US-09-724-676A-71847
7	57	87.7	388	6	US-10-236-392-34
8	57	87.7	481	6	US-10-236-392-36
9	57	87.7	644	1	PCT-US02-37760-5
10	57	87.7	644	6	US-10-236-392-32
11	57	87.7	866	1	PCT-US02-37760-6
12	57	87.7	866	5	US-09-949-002-302
13	57	87.7	875	5	US-09-949-002-455
14	46	70.8	17	6	US-10-293-580-45
15	40	61.0	289	6	US-10-310-154-381
16	39	60.0	286	5	US-09-950-054-5126
17	38	58.5	115	5	US-09-513-999C-5898
18	38	58.5	320	5	US-09-724-676-62455
19	38	58.5	320	5	US-09-724-676-62455
20	38	58.5	325	5	US-09-724-676-62456
21	38	58.5	325	5	US-09-724-676A-62456
22	38	58.5	608	1	PCT-US02-35563-27
23	38	58.5	611	6	US-10-223-089-340
24	38	58.5	671	5	US-09-724-676-62453
25	38	58.5	671	5	US-09-724-676A-62453
26	38	58.5	671	5	US-09-724-676-62454

27 38 58.5 676 5 US-09-724-676A-62454 Sequence 62454, A
28 38 58.5 722 5 US-09-724-676-62452 Sequence 62452, A
29 38 58.5 722 5 US-09-724-676A-62452 Sequence 62452, A
30 37 56.9 381 6 US-10-099-056-1416 Sequence 1416, Ap
31 36 55.4 11 6 US-10-212-499-39 Sequence 39, Appl
32 36 55.4 175 6 US-10-264-237-1928 Sequence 1928, Ap
33 36 55.4 311 5 US-09-724-676-75821 Sequence 75821, A
34 36 55.4 311 5 US-09-724-676A-75821 Sequence 75821, A
35 36 55.4 426 6 US-10-203-138A-13561 Sequence 13561, A
36 36 55.4 500 6 US-10-288-798-4 Sequence 4, Appl
37 36 55.4 611 7 US-60-428-082-19 Sequence 19, Appl
38 36 55.4 1268 6 US-10-276-774-2166 Sequence 2166, Ap
39 36 55.4 1472 5 US-09-724-676-57022 Sequence 57022, A
40 36 55.4 1472 5 US-09-724-676-57022 Sequence 57022, A
41 36 55.4 1493 5 US-09-724-676-57021 Sequence 57021, A
42 36 55.4 1493 5 US-09-724-676A-57021 Sequence 57021, A
43 36 55.4 1583 1 PCT-US02-32727-15149 Sequence 15149, A
44 36 55.4 1583 6 US-10-057-498-15149 Sequence 15149, A
45 36 55.4 1783 6 US-10-275-140-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-09-845-729-1
; Sequence 1, Application US/09845729
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; FILE REFERENCE: 2132.031
; CURRENT APPLICATION NUMBER: US/09/845,729
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-729-1

Query Match 100.0%; Score 65; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SESDFLAGGGVR 13
Db 1 SESDFLAGGGVR 13

RESULT 2

US-10-325-162-1
; Sequence 1, Application US/10325162
; GENERAL INFORMATION:
; APPLICANT: Kupchak, Peter
; APPLICANT: Marshall, John
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: Method of Confirming the Presence of Myocardial Infarction
; FILE REFERENCE: 2132.132
; CURRENT APPLICATION NUMBER: US/10/325,162
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-325-162-1

Query Match 87.7%; Score 57; DB 6; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.0085;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| | | | | | | | | |
Db 5 EGDFLAEGGGVR 16

RESULT 3

US-09-724-676-71849
; Sequence 71849, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71849
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-71849

Query Match 87.7%; Score 57; DB 5; Length 70;
Best Local Similarity 91.7%; Pred. No. 0.034;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| | | | | | | | | |
Db 24 EGDFLAEGGGVR 35

RESULT 4

US-09-724-676A-71849
; Sequence 71849, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71849
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-71849

Query Match 87.7%; Score 57; DB 5; Length 70;
Best Local Similarity 91.7%; Pred. No. 0.034;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| | | | | | | | | |
Db 24 EGDFLAEGGGVR 35

RESULT 5

US-09-724-676-71847
; Sequence 71847, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71847
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-724-676-71847

Query Match 87.7%; Score 57; DB 5; Length 93;
Best Local Similarity 91.7%; Pred. No. 0.045;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| | | | | | | | | |
Db 42 EGDFLAEGGGVR 53

RESULT 6

US-09-724-676A-71847
; Sequence 71847, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71847
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-71847

Query Match 87.7%; Score 57; DB 5; Length 93;
Best Local Similarity 91.7%; Pred. No. 0.045;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| | | | | | | | | |
Db 42 EGDFLAEGGGVR 53

RESULT 7

US-10-236-392-34
; Sequence 34, Application US/10236392
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaBouchelle, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A


```

; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 34
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-34

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Query Match      87.7%  Score 57; DB 6; Length 388;
Best Local Similarity 91.7%  Pred. No. 0.18;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2  ESDFLAEGGGVR 13
      |  |||||
Db      24  EGDFLAEGGGVR 35

```

```

RESULT 8
US-10-236-392-36
; Sequence 36, Application US/10236392
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladamir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRoche, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A

```

```

; APPLICANT: Smithsonian, Glennda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 36
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-36

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```

Query Match      87.7%  Score 57; DB 6; Length 481;
Best Local Similarity 91.7%  Pred. No. 0.21;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Qy      2  ESDFLAEGGGVR 13
      |  |||||
Db      24  EGDFLAEGGGVR 35

```

```

RESULT 9
PCT-US02-37760-5
; Sequence 5, Application PC/TUS0237760
; GENERAL INFORMATION:
; APPLICANT: GENVEC, INC.
; APPLICANT: KESSLER, PAUL D
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: ANGIOPOIETIN RELATED FACTORS
; FILE REFERENCE: 220091
; CURRENT APPLICATION NUMBER: PCT/US02/37760
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/334488
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-37760-5

```

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Query Match      87.7%  Score 57; DB 1; Length 644;
Best Local Similarity 91.7%  Pred. No. 0.28;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      2  ESDFLAEGGGVR 13
      |  |||||
Db      24  EGDFLAEGGGVR 35

```

```

Db      24  EGDFLAEGGGVR  35

RESULT 11
PCT-US02-37760-6
; Sequence 6, Application PC/TUS0237760
; GENERAL INFORMATION:
; APPLICANT: GENVEC, INC.
; APPLICANT: KESSLER, PAUL D
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: ANGIOPOIETIN RELATED FACTORS
; FILE REFERENCE: 220091
; CURRENT APPLICATION NUMBER: PCT/US02/37760
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/334488
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 866
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-37760-6

Query Match      87.7%; Score 57; DB 1; Length 866;
Best Local Similarity 91.7%; Pred. No. 0.38;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  ESDFLAEGGGVR  13
| | | | | | | | | |
Db      24  EGDFLAEGGGVR  35

RESULT 12
US-09-949-002-302
; Sequence 302, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 866
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-302

Query Match      87.7%; Score 57; DB 5; Length 866;
Best Local Similarity 91.7%; Pred. No. 0.38;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  ESDFLAEGGGVR  13
| | | | | | | | | |
Db      24  EGDFLAEGGGVR  35

RESULT 13
US-09-949-002-455
; Sequence 455, Application US/09949002
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002

```

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; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 455
; LENGTH: 875
; TYPE: PRT
; ORGANISM: Human
US-09-949-002-455

Query Match      87.7%; Score 57; DB 5; Length 875;
Best Local Similarity 91.7%; Pred. No. 0.38;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2  ESDFLAEGGGVR 13
Db  33  EGDFLAEGGGVR 44

RESULT 14
US-10-293-580-45
; Sequence 45, Application US/10293580
; GENERAL INFORMATION:
; APPLICANT: Aurora Biosciences Corporation
; TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
; FILE REFERENCE: AU01270 (08366/031001)
; CURRENT APPLICATION NUMBER: US/10/293,580
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/129,192
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: thrombin
US-10-293-580-45

Query Match      70.8%; Score 46; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  5  FLAEGGGVR 13
Db  1  FLAEGGGVR 9

RESULT 15
US-10-310-154-381
; Sequence 381, Application US/10310154
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Chomet, Paul S.
; APPLICANT: Adams, Thomas H
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Agarwal, Aneeta K.
; APPLICANT: Ahrens, Jeffrey E.
; APPLICANT: Ball, James A.
; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Molian
; APPLICANT: Dong, Jinzhao
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshieh
; APPLICANT: Johnson, G. Richard
```

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; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jingdong
; APPLICANT: Lu, Bin
; APPLICANT: Luethy, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Malloy, Kathleen A.
; APPLICANT: McKiel, Christine D.
; APPLICANT: Miller, Philip W.
; APPLICANT: Padmavathi, Manchikanti
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Start, William G.
; APPLICANT: Tennesen, Dan
; APPLICANT: Vidya, K.R.
; APPLICANT: Wang, Haiyun
; APPLICANT: Xin, Zhanguo
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zeng, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhao, Yajuan
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 39-15(52796)B
; CURRENT APPLICATION NUMBER: US/10/310,154
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 381
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Zea mays
US-10-310-154-381

Query Match      61.5%; Score 40; DB 6; Length 489;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy  1  SESDFLAEGGGVR 13
Db  419  TSKDFMAFGGGLR 431

Search completed: February 10, 2003, 16:14:54
Job time : 61 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 10, 2003, 15:55:46 ; Search time 82 Seconds
(without alignments)
21.125 Million cell updates/sec

Title: US-09-845-729-1

Perfect score: 65

Sequence: 1 SESDFLAEGGGVR 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	87.7	16	17 AAR96194	Fibrinogen epitope
2	57	87.7	16	18 AAR96194	Fibrinogen epitope
3	57	87.7	16	20 AAR96194	Antimicrobial pept
4	57	87.7	16	22 AAR96194	Antimicrobial pept
5	57	87.7	16	22 AAR96194	Vascular dementia
6	57	87.7	16	22 AAR96194	Human API-118 tryp
7	57	87.7	16	22 AAR96194	Fibronectin fragme
8	57	87.7	17	22 AAR96194	Fibrinogen epitope
9	57	87.7	17	22 AAR96194	Fibronectin fragme
10	57	87.7	19	17 AAR96192	Fibrinogen epitope

11	57	87.7	20	17 AAR96191	Fibrinogen epitope
12	57	87.7	20	20 AAR96191	Antimicrobial pept
13	57	87.7	21	17 AAR96183	Fibrinogen epitope
14	57	87.7	22	10 AAR96182	Antigen probe for
15	57	87.7	22	17 AAR96182	Fibrinogen epitope
16	57	87.7	22	17 AAR96190	Fibrinogen epitope
17	57	87.7	24	23 AAR96190	Anti-angiogenic al
18	57	87.7	24	23 AAR96190	Anti-angiogenic al
19	57	87.7	24	23 AAR96190	Anti-angiogenic al
20	57	87.7	24	23 AAR96190	Anti-angiogenic al
21	57	87.7	24	23 AAR96190	Anti-angiogenic al
22	57	87.7	24	23 AAR96190	Anti-angiogenic al
23	57	87.7	24	23 AAR96190	Anti-angiogenic al
24	57	87.7	25	23 AAR96190	Anti-angiogenic al
25	57	87.7	25	23 AAR96190	Anti-angiogenic al
26	57	87.7	25	23 AAR96190	Anti-angiogenic al
27	57	87.7	25	23 AAR96190	Anti-angiogenic al
28	57	87.7	25	23 AAR96190	Anti-angiogenic al
29	57	87.7	25	23 AAR96190	Anti-angiogenic al
30	57	87.7	25	23 AAR96190	Anti-angiogenic al
31	57	87.7	25	23 AAR96190	Anti-angiogenic al
32	57	87.7	25	23 AAR96190	Anti-angiogenic al
33	57	87.7	25	23 AAR96190	Anti-angiogenic al
34	57	87.7	25	23 AAR96190	Anti-angiogenic al
35	57	87.7	25	23 AAR96190	Anti-angiogenic al
36	57	87.7	25	23 AAR96190	Anti-angiogenic al
37	57	87.7	25	23 AAR96190	Anti-angiogenic al
38	57	87.7	25	23 AAR96190	Anti-angiogenic al
39	57	87.7	25	23 AAR96190	Anti-angiogenic al
40	57	87.7	25	23 AAR96190	Anti-angiogenic al
41	57	87.7	25	23 AAR96190	Anti-angiogenic al
42	57	87.7	25	23 AAR96190	Anti-angiogenic al
43	57	87.7	25	23 AAR96190	Anti-angiogenic al
44	57	87.7	25	23 AAR96190	Anti-angiogenic al
45	57	87.7	25	23 AAR96190	Anti-angiogenic al

ALIGNMENTS

RESULT 1

AAR96194
ID AAR96194 standard; peptide; 16 AA.

XX AAR96194;

XX 19-DEC-1996 (first entry)

DT Fibrinogen epitope probe, represents alpha chain residues 1-16.

DE Epitope: cleavage product; human; leukocyte elastase; HLE; fibrinogen;
KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
KW sputum; bronchoalveolar lavage fluid; assay; inhibitor; arthritis;
KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
KW chronic obstructive pulmonary disease; myelogenous leukaemia;
KW infantile respiratory distress syndrome; gout;
KW adult respiratory distress syndrome.

XX Homo sapiens.

XX WO9614580-A1.

XX 17-MAY-1996.

XX 03-NOV-1995; 95WO-US13794.

XX 06-JUN-1995; 95US-0469141.

XX 07-NOV-1994; 94US-0335524.

XX (MERI) MERCK & CO INC.

XX Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;

DR WPI; 1996-251888/25.
 XX New isolated fibrinogen derived cleavage products - used for
 PT detection of leukocyte elastase activity in disease diagnosis and
 PT for evaluating elastase inhibitors
 XX Example 5; Page 42; 109pp; English.
 XX The sequences given in AAR96182-94 represent antigenic probes derived
 CC from the first 21 amino acids of human fibrinogen. These probes are
 CC used to determine antibody titre against other fibrinogen cleavage
 CC products. The monospecific antibodies may be used to assay for the
 CC formation of complementary cleavage product antigens or epitopes in
 CC whole blood or other body fluids, peritoneal fluid, sputum or
 CC bronchoalveolar lavage fluid. The assay for cleavage products is
 CC dependent upon the presence of HLE in the sample. This assay can also
 CC be used for the evaluation of HLE inhibitors. The antibodies may be
 CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
 CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
 CC pulmonary disease, bronchiectasis, adult or infantile respiratory
 CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.
 XX Sequence 16 AA;
 SQ

Query Match 87.7%; Score 57; DB 17; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.004;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ESDFLAEGGGVR 13
 Db | | | | | | | | | |
 5 EGDFLAEGGGVR 16

RESULT 2
 AAW04619
 ID AAW04619 standard; peptide; 16 AA.
 AC AAW04619;
 XX
 DT 13-AUG-1997 (first entry)
 XX
 DE Fibrinopeptide A peptide for mass spectrometry analysis.
 XX
 KW Mass spectrometry; polymer analysis; biopolymer analysis.
 XX
 OS Synthetic.
 XX
 PN WO9636986-A1.
 XX
 PD 21-NOV-1996.
 XX
 PF 17-MAY-1996; 96WO-US07146.
 XX
 PR 19-MAY-1995; 95US-0447175.
 PR 19-MAY-1995; 95US-0446055.
 XX
 PA (PERS-) PERSEPTIVE BIOSYSTEMS INC.
 XX
 PI Patterson DH, Tarr GE;
 XX
 DR WPI; 1997-012308/01.
 XX
 PT Sequencing polymers, e.g. DNA, RNA, peptide nucleic acids, proteins,
 PT etc. - by obtaining mass to charge ratios of polymer fragments,
 PT pref. using mass spectrometer, and performing statistical analysis
 XX
 XX Example 2; Page 32; 86pp; English.
 PS
 CC A method of obtaining sequence information about a polymer (e.g. DNA,
 CC RNA, peptide nucleic acids, proteins, peptides and carbohydrates)
 CC comprising monomers of known mass has been claimed. The present
 CC sequence represents a fibrinopeptide A peptide, and was used as
 CC an example as a digestion before analysis by mass spectrometry,
 CC

CC using this novel on-plate strategy. Total sequence information
 CC from a nine well digestion can be represented in a single digestion or
 CC it is often derived from two or more wells. The methods, apparatus and
 CC kit (claimed) can be used for the analysis of polymers, particularly
 CC biopolymers, e.g. DNA, RNA, peptide nucleic acids, proteins, peptides
 CC and carbohydrates. It provides a rapid, automated and cost effective
 CC sequencing of polymers, with a statistical certainty.
 XX
 SQ Sequence 16 AA;
 Query Match 87.7%; Score 57; DB 18; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.004;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ESDFLAEGGGVR 13
 Db | | | | | | | | | |
 5 EGDFLAEGGGVR 16

RESULT 3
 AAY57487
 ID AAY57487 standard; Peptide; 16 AA.
 XX
 AC AAY57487;
 XX
 DT 25-FEB-2000 (first entry)
 XX
 DE Antimicrobial peptide CS-FBP-alpha SEQ ID NO:25.
 XX
 KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
 KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
 XX
 OS Synthetic.
 OS Oryctolagus cuniculus.
 XX
 PN WO9942119-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 17-FEB-1999; 99WO-US03350.
 XX
 PR 18-FEB-1998; 98US-0025319.
 XX
 PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
 XX
 PI Yeaman MR, Shen AJ;
 XX
 DR WPI; 1999-527417/44.
 XX
 PT Antimicrobial peptides for potentiating antimicrobial agents active
 PT against bacteria and fungi -
 XX
 PS Disclosure; Page 120; 166pp; English.
 XX
 CC The present invention describes an antimicrobial peptide (AP) for direct
 CC activity or for potentiating antimicrobial agents active against
 CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
 CC containing an amino acid sequence selected from the group consisting
 CC essentially of a first peptide template XZBZBXXB and its derivatives
 CC selected from XZBZBXXB, BXZXB, BXZXXB, XBBZXXB and BXXZBXXZ; and
 CC (b) a second peptide template XBXX and their derivatives selected from
 CC the group consisting of XBXXB, XBXXB, BXBXBX, XBBXXB, and
 CC XBZXXBXXZBXX; where B = at least one positively charged amino acid;
 CC X = at least one non-polar hydrophobic amino acid; Z = at least one
 CC aromatic amino acid, and where B, X and Z may be separated by one or
 CC more other amino acids. The peptides can be used to treat bacterial and
 CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 20; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.004;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 4

ABB56219
 ID ABB56219 standard; Peptide; 16 AA.

XX AC ABB56219;

XX DT 15-FEB-2002 (first entry)

XX DE Vascular dementia-associated protein isoform (VPI) 419.

XX KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
 XX KW diagnosis; prognosis; gene therapy.

XX OS Homo sapiens.

XX PN WO200169261-A2.

XX PD 20-SEP-2001.

XX PF 14-MAR-2001; 2001WO-GB01106.

XX PR 15-MAR-2000; 2000GB-0006285.

XX PR 24-NOV-2000; 2000GB-0028734.

XX PR 28-NOV-2000; 2000US-0724391.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Herath HMAC, Parekh RB, Rohlf C;

XX DR WPI; 2001-557937/62.

XX PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 PT determining stage of VD and monitoring the effect of VD therapy, for
 PT comprises analysing body fluid by 2-dimensional electrophoresis, for
 PT features correlated with VD -

XX PS Claim 6; Page 39; i5lpp; English.

XX CC The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for
 CC monitoring the effect of therapy administered to a subject having VD.
 CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are
 CC useful for the treatment of VD and for gene therapy.

XX SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 22; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.004;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 5

ABB52337
 ID ABB52337 standard; Peptide; 16 AA.

XX AC ABB52337;

XX DT 08-FEB-2002 (first entry)

XX DE Human API-118 tryptic digest peptide #2.

XX KW Human; neuroprotective; nootropic; gene therapy; vaccine;

XX KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;

XX KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;

XX KW Expression Reference Protein Isoform; ERPI; proteolysis.

XX OS Homo sapiens.

XX PN WO200175454-A2.

XX PD 11-OCT-2001.

XX PF 03-APR-2001; 2001WO-US10908.

XX PR 03-APR-2000; 2000US-194504P.

XX PR 28-NOV-2000; 2000US-253647P.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PF (PFIZ) PFIZER INC.

XX PI Durham KL, Friedman DL, Herath HMAC, Kimmel LH, Parekh RB;

XX PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;

XX PI Townsend RR, White F, Williams SA;

XX DR WPI; 2001-639384/73.

XX PT Screening for Alzheimer's disease in a mammal, by making
 PT two-dimensional array of a feature whose relative abundance correlates
 PT with disease, and comparing with abundance of the feature in samples of
 PT healthy persons -

XX PS Example; Page 33; 162pp; English.

XX CC The invention relates to methods for the screening, diagnosis and
 CC prognosis of Alzheimer's disease. The methods involve the detection
 CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's
 CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,
 CC serum or plasma. The abundance of the AFs and APIs is then
 CC normalised to an Expression Reference Protein Isoform (ERPI) in
 CC order to determine whether a patient is suffering from, or has
 CC a predisposition to, Alzheimer's Disease. The relative abundance of
 CC the AFs and APIs correlates with the severity of Alzheimer's Disease.
 CC The present sequence is a peptide produced from an API by proteolysis.

XX SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 22; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.004;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 6

AAAB91959
 ID AAAB91959 standard; Peptide; 16 AA.

XX AC AAAB91959;

XX DT 22-JUN-2001 (first entry)

XX DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1135.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US13576.
 XX
 PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT
 XX
 PS Disclosure; Page 567; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 16 AA;
 Query Match 87.7%; Score 57; DB 22; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.004;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16
 RESULT 7
 AAB96184
 ID AAB96184 standard; peptide; 17 AA.
 XX
 AC AAB96184;
 XX
 DT 19-DEC-1996 (first entry)
 XX
 DE Fibrinogen epitope probe, represents alpha chain residues 5-21.
 XX
 KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
 KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
 KW sputum; bronchoalveolar lavage fluid; assay; inhibitor; arthritis;
 KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;

KW chronic obstructive pulmonary disease; myelogenous leukaemia;
 KW infantile respiratory distress syndrome; gout;
 KW adult respiratory distress syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO9614580-A1.
 XX
 PD 17-MAY-1996.
 XX
 PF 03-NOV-1995; 95WO-US13794.
 XX
 PR 06-JUN-1995; 95US-0469141.
 PR 07-NOV-1994; 94US-0335524.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;
 XX
 DR WPI; 1996-251888/25.
 XX
 PT New isolated fibrinogen derived cleavage products - used for
 PT detection of leukocyte elastase activity in disease diagnosis and
 PT for evaluating elastase inhibitors
 XX
 PS Example 5; Page 41; 109pp; English.
 XX
 CC The sequences given in AAB96182-94 represent antigenic probes derived
 CC from the first 21 amino acids of human fibrinogen. These probes are
 CC used to determine antibody titre against other fibrinogen cleavage
 CC products. The monospecific antibodies may be used to assay for the
 CC formation of complementary cleavage product antigens or epitopes in
 CC whole blood or other body fluids, peritoneal fluid, sputum or
 CC bronchoalveolar lavage fluid. The assay for cleavage products is
 CC dependent upon the presence of HLE in the sample. This assay can also
 CC be used for the evaluation of HLE inhibitors. The antibodies may be
 CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
 CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
 CC pulmonary disease, bronchiectasis, adult or infantile respiratory
 CC distress syndrome and myelogenous leukaemia. See also AAB96146-81.
 XX
 SQ Sequence 17 AA;
 Query Match 87.7%; Score 57; DB 17; Length 17;
 Best Local Similarity 91.7%; Pred. No. 0.0043;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 1 EGDFLAEGGGVR 12
 RESULT 8
 AAB91960
 ID AAB91960 standard; Peptide; 17 AA.
 XX
 AC AAB91960;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Fibrinectin fragment and fibrin related peptide SEQ ID NO:1136.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX

DR WPI; 1996-251888/25.

XX New isolated fibrinogen derived cleavage products - used for

PT detection of leukocyte elastase activity in disease diagnosis and

PT for evaluating elastase inhibitors

XX Example 5; Page 42; 109pp; English.

PS The sequences given in AAR96182-94 represent antigenic probes derived

CC from the first 21 amino acids of human fibrinogen. These probes are

CC used to determine antibody titre against other fibrinogen cleavage

CC products. The monospecific antibodies may be used to assay for the

CC formation of complementary cleavage product antigens or epitopes in

CC whole blood or other body fluids, peritoneal fluid, sputum or

CC bronchoalveolar lavage fluid. The assay for cleavage products is

CC dependent upon the presence of HLE in the sample. This assay can also

CC be used for the evaluation of HLE inhibitors. The antibodies may be

CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary

CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive

CC pulmonary disease, bronchiectasis, adult or infantile respiratory

CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.

XX Sequence 19 AA;

SQ Query Match 87.7%; Score 57; DB 17; Length 19;
Best Local Similarity 91.7%; Pred. NO. 0.0048;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
| | | | | | | | | |
DB 5 EGDFLAEGGGVR 16

RESULT 11

AAR96191

ID AAR96191 standard; peptide; 20 AA.

XX AC AAR96191;

XX DT 19-DEC-1996 (first entry)

XX DE Fibrinogen epitope probe, represents alpha chain residues 1-20.

XX KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;

XX KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;

XX KW sputum; bronchoalveolar lavage fluid; assay; inhibitor; arthritis;

XX KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;

XX KW chronic obstructive pulmonary disease; myelogenous leukaemia;

XX KW infantile respiratory distress syndrome; gout;

XX KW adult respiratory distress syndrome.

XX OS Homo sapiens.

XX PN WO9614580-A1.

XX PD 17-MAY-1996.

XX PF 03-NOV-1995; 95WO-US13794.

XX PR 06-JUN-1995; 95US-0469141.

XX PR 07-NOV-1994; 94US-0335524.

XX PA (MERI) MERCK & CO INC.

XX PI Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;

XX WPI; 1996-251888/25.

XX New isolated fibrinogen derived cleavage products - used for

PT detection of leukocyte elastase activity in disease diagnosis and

PT for evaluating elastase inhibitors

XX Example 5; Page 42; 109pp; English.

XX The sequences given in AAR96182-94 represent antigenic probes derived

CC from the first 21 amino acids of human fibrinogen. These probes are

CC used to determine antibody titre against other fibrinogen cleavage

CC products. The monospecific antibodies may be used to assay for the

CC formation of complementary cleavage product antigens or epitopes in

CC whole blood or other body fluids, peritoneal fluid, sputum or

CC bronchoalveolar lavage fluid. The assay for cleavage products is

CC dependent upon the presence of HLE in the sample. This assay can also

CC be used for the evaluation of HLE inhibitors. The antibodies may be

CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary

CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive

CC pulmonary disease, bronchiectasis, adult or infantile respiratory

CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.

XX Sequence 20 AA;

SQ Query Match 87.7%; Score 57; DB 17; Length 20;
Best Local Similarity 91.7%; Pred. NO. 0.0051;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
| | | | | | | | | |
DB 5 EGDFLAEGGGVR 16

RESULT 12

AAAY57488

ID AAY57488 standard; Peptide; 20 AA.

XX AC AAY57488;

XX DT 25-FEB-2000 (first entry)

XX DE Antimicrobial peptide CS-FBP-alpha-TET SEQ ID NO:26.

XX KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;

XX KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.

XX OS Synthetic.

XX OS Oryctolagus cuniculus.

XX PN WO9942119-A1.

XX PD 26-AUG-1999.

XX PF 17-FEB-1999; 99WO-US03350.

XX PR 18-FEB-1998; 98US-0025319.

XX PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.

XX PI Yeaman MR, Shen AJ;

XX WPI; 1999-527417/44.

XX Antimicrobial peptides for potentiating antimicrobial agents active

PT against bacteria and fungi -

XX Disclosure; Page 120; 166pp; English.

XX The present invention describes an antimicrobial peptide (AP) for direct

CC activity or for potentiating antimicrobial agents active against

CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide

CC containing an amino acid sequence selected from the group consisting

CC essentially of a first peptide template XZBZXBXB and its derivatives

CC selected from XZBZXBXBXB, BXZXB, BXZXZXB, XBXZXBXB and BBZXZBXZ; and

CC (b) a second peptide template XBBXX and their derivatives selected from

CC the group consisting of XBBXBBX, XBBXBBX, BXXBXXB, XBBZXBB, and

CC XBBZXBBXBBX; where B = at least one positively charged amino acid;

CC X = at least one non-polar hydrophobic amino acid; Z = at least one

CC aromatic amino acid, and where B, X and Z may be separated by one or

CC more other amino acids. The peptides can be used to treat bacterial and

CC fungal infections. The peptides also increase the antimicrobial activity
 CC of neutrophils. The peptides overall effect cellular disruption and
 CC rapid apoptosis of microbial cells. AAY57463 to AAY57557 represent
 CC sequences used in the exemplification of the present invention.

XX SQ Sequence 20 AA;

Query Match 87.7%; Score 57; DB 20; Length 20;
 Best Local Similarity 91.7%; Pred. No. 0.0051;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 13

ID AAR96183 standard; peptide; 21 AA.

XX AAR96183;

XX 19-DEC-1996 (first entry)

XX Fibrinogen epitope probe, represents alpha chain residues 1-21.

XX Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
 KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
 KW sputum; bronchoalveolar lavage fluid; assay; inhibitor; arthritis;
 KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
 KW chronic obstructive pulmonary disease; myelogenous leukaemia;
 KW infantile respiratory distress syndrome; gout;
 KW adult respiratory distress syndrome.

XX Homo sapiens.

XX WO9614580-A1.

XX 17-MAY-1996.

XX 03-NOV-1995; 95WO-US13794.

XX 06-JUN-1995; 95US-0469141.

XX 07-NOV-1994; 94US-0335524.

XX (MERI) MERCK & CO INC.

XX Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;

XX WPI; 1996-251888/25.

XX New isolated fibrinogen derived cleavage products - used for
 PT detection of leukocyte elastase activity in disease diagnosis and
 PT for evaluating elastase inhibitors

XX Example 5; Page 41; 109pp; English.

XX The sequences given in AAR96182-94 represent antigenic probes derived
 CC from the first 21 amino acids of human fibrinogen. These probes are
 CC used to determine antibody titre against other fibrinogen cleavage
 CC products. The monospecific antibodies may be used to assay for the
 CC formation of complementary cleavage product antigens or epitopes in
 CC whole blood or other body fluids, peritoneal fluid, sputum or
 CC bronchoalveolar lavage fluid. The assay for cleavage products is
 CC dependent upon the presence of HLE in the sample. This assay can also
 CC be used for the evaluation of HLE inhibitors. The antibodies may be
 CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
 CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
 CC pulmonary disease, bronchiectasis, adult or infantile respiratory
 CC distress syndrome and myelogenous leukaemia. See also AAR96146-81.

XX Sequence 21 AA;

Query Match 87.7%; Score 57; DB 17; Length 21;
 Best Local Similarity 91.7%; Pred. No. 0.0054;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 14

ID AAP90276 standard; protein; 22 AA.

XX AAP90276;

XX 17-MAY-1990 (first entry)

XX Antigen probe for human fibrinogen C-terminal alpha chain cleavage prods.

XX C-terminal; antigenic peptide; fibrinogen; human leukocyte elastase;
 CC connective tissue disease; alpha chain; probe;

XX Homo sapiens.

XX EP345906-A.

XX 13-DEC-1989.

XX 07-JUN-1989; 89EP-0201460.

XX 10-JUN-1988; 88US-0205416.

XX 10-JUN-1988; 88US-0205417.

XX 10-JUN-1988; 88US-0205418.

XX (MERI) MERCK AND CO. INC.

XX Dahlgren ME, Mumford RA, Boger JS, Davies DTP;

XX WPI; 1989-365672/50.

XX New elastase-induced fibrinogen cleavage peptide(s) - for prodn. of

XX new diagnostic antibodies.

XX Example 5; page 17; 33pp; English.

XX The synthetic peptide corresponds to AAs 1-22 of human fibrinogen alpha
 CC chain. Probes with a tyrosine at the N-terminal (distal to the epitope)
 CC for coupling to 125. Probes may also be used to determine to evaluate the
 CC presence and amt. of human leukocyte elastase (HLE) cleavage prods. of
 CC human fibrinogen. Truncated versions of this sequence, eg AAs 5-21,
 CC 9-21, 12-21, 14-21, 15-21, or 17-21; or 1-21,22,20,19,18, or 16 are used
 CC to determine antibody specificity and demonstrate that the specificity
 CC resides in AAs 17-21. HLE-induced cleavage of hp occurs in eg
 CC connective tissue destructive diseases such as emphysema, chronic
 CC bronchitis, cystic fibrosis, arthritis, psoriasis, or atherosclerosis.

XX Sequence 22 AA;

Query Match 87.7%; Score 57; DB 10; Length 22;
 Best Local Similarity 91.7%; Pred. No. 0.0056;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 15

ID AAR96182 standard; peptide; 22 AA.

XX AAR96182;

XX

DT 19-DEC-1996 (first entry)
XX Fibrinogen epitope probe, represents alpha chain residues -1-21.
DE
XX Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
XX monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
KW sputum; bronchoalveolar lavage fluid; assay; inhibitor; arthritis;
KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
KW chronic obstructive pulmonary disease; myelogenous leukaemia;
KW infantile respiratory distress syndrome; gout;
KW adult respiratory distress syndrome.
XX
OS Homo sapiens.
XX
XX WO9614580-A1.
XX
XX 17-MAY-1996.
PD
XX 03-NOV-1995; 95WO-US13794.
XX
XX 06-JUN-1995; 95US-0469141.
XX
XX 07-NOV-1994; 94US-0335524.
PR
XX (MERI) MERCK & CO INC.
FA
XX Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;
XX WPI; 1996-251888/25.
XX
XX New isolated fibrinogen derived cleavage products - used for
PT detection of leukocyte elastase activity in disease diagnosis and
PT for evaluating elastase inhibitors
XX
XX Example 5; Page 41; 109pp; English.
PS
XX The sequences given in AAR96182-94 represent antigenic probes derived
CC from the first 21 amino acids of human fibrinogen. These probes are
CC used to determine antibody titre against other fibrinogen cleavage
CC products. The monospecific antibodies may be used to assay for the
CC formation of complementary cleavage product antigens or epitopes in
CC whole blood or other body fluids, peritoneal fluid, sputum or
CC bronchoalveolar lavage fluid. The assay for cleavage products is
CC dependent upon the presence of HLE in the sample. This assay can also
CC be used for the evaluation of HLE inhibitors. The antibodies may be
CC used to diagnose and monitor diseases such as arthritis, gout, pulmonary
CC emphysema, chronic bronchitis, cystic fibrosis, chronic obstructive
CC pulmonary disease, bronchiectasis, adult or infantile respiratory
XX distress syndrome and myelogenous leukaemia. See also AAR96146-81.
XX
SQ Sequence 22 AA;
Query Match 87.7%; Score 57; DB 17; Length 22;
Best Local Similarity 91.7%; Pred.No. 0.0056;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 ESDFLAEGGGVR 13
| | | | | | | | | |
Db 6 EGDFLAEGGGVR 17
Search completed: February 10, 2003, 16:00:48
Job time : 83 secs

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OM protein - protein search, using sw model

Run on: February 10, 2003, 15:59:27 ; Search time 15 Seconds
(without alignments)
25.500 Million cell updates/sec

Title: US-09-845-729-1

Perfect score: 65

Sequence: 1 SESDFLAGGGVR 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	87.7	16	2	US-08-796-598-14
2	57	87.7	16	2	US-08-447-175A-14
3	57	87.7	16	3	US-08-469-141A-56
4	57	87.7	16	5	PCT-US95-13794-56
5	57	87.7	17	3	US-08-469-141A-46
6	57	87.7	17	5	PCT-US95-13794-46
7	57	87.7	18	3	US-08-469-141A-55
8	57	87.7	18	5	PCT-US95-13794-55
9	57	87.7	19	3	US-08-469-141A-54
10	57	87.7	19	5	PCT-US95-13794-54
11	57	87.7	20	1	US-08-288-657-1
12	57	87.7	20	1	US-07-984-884-1
13	57	87.7	20	1	US-08-481-810-1
14	57	87.7	20	1	US-08-484-426-1
15	57	87.7	20	2	US-08-480-818-1
16	57	87.7	20	3	US-08-469-141A-53
17	57	87.7	20	5	PCT-US95-13794-53
18	57	87.7	21	3	US-08-469-141A-45
19	57	87.7	21	5	PCT-US95-13794-45
20	57	87.7	22	3	US-08-469-141A-44
21	57	87.7	22	3	US-08-469-141A-52
22	57	87.7	22	5	PCT-US95-13794-44
23	57	87.7	22	5	PCT-US95-13794-52
24	57	87.7	23	4	US-08-860-808E-25
25	57	87.7	25	4	US-08-440-322-16
26	57	87.7	25	4	US-08-440-331-16
27	57	87.7	30	2	US-07-963-538B-9

28	57	87.7	643	2	US-08-551-356-4	Sequence 4, Appli
29	57	87.7	643	5	PCT-US93-12687-4	Sequence 4, Appli
30	57	87.7	644	1	US-08-206-176-2	Sequence 2, Appli
31	57	87.7	847	4	US-09-373-157-4	Sequence 4, Appli
32	52	80.0	15	3	US-08-469-141A-6	Sequence 6, Appli
33	52	80.0	15	5	PCT-US95-13794-6	Sequence 6, Appli
34	52	80.0	28	6	5196404-16	Patent No. 5196404
35	47	72.3	10	6	5196404-18	Patent No. 5196404
36	47	72.3	10	6	5433940-25	Patent No. 5433940
37	46	70.8	17	2	US-08-792-553-11	Sequence 11, Appl
38	46	70.8	24	2	US-08-978-404B-48	Sequence 48, Appl
39	40	61.5	13	3	US-08-469-141A-47	Sequence 47, Appl
40	40	61.5	13	5	PCT-US95-13794-47	Sequence 47, Appl
41	36	55.4	11	3	US-08-592-500-39	Sequence 39, Appl
42	36	55.4	11	3	US-08-195-006-39	Sequence 39, Appl
43	36	55.4	11	5	PCT-US94-07644A-39	Sequence 39, Appl
44	36	55.4	14	4	US-08-860-808E-1	Sequence 1, Appli
45	36	55.4	420	1	US-08-391-259-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-08-796-598-14
; Sequence 14, Application US/08796598
; Patent No. 5827659
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, DALE H.
; APPLICANT: TARR, GEORGE E.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Patent Administrator - Testa, Hurwitz &
; ADDRESSEE: Thibault
; STREET: High Street Tower, 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,598
; FILING DATE: 07-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,055
; FILING DATE: 19-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FLYNN Esq., Kerry A.
; REGISTRATION NUMBER: 33,693
; REFERENCE/DOCKET NUMBER: SYP-115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-796-598-14

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00089;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
| | | | |
Db 5 EGDFLAEGGGVR 16

RESULT 2

US-08-447-175A-14
; Sequence 14, Application US/08447175A
; Patent No. 5869240
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, DALE H.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
; TITLE OF INVENTION: POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
; TITLE OF INVENTION: SPECTROMETRY.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Administrator - Testa, Hurwitz &
; ADDRESSEE: Thibault, LLP
; STREET: High Street Tower, 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,175A
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 422
; ATTORNEY/AGENT INFORMATION:
; NAME: RAUSCHENBACH, Kurt
; REGISTRATION NUMBER: 40,137
; REFERENCE/DOCKET NUMBER: SYP-114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-447-175A-14

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00089;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
| | | | |
Db 5 EGDFLAEGGGVR 16

RESULT 3

US-08-469-141A-56
; Sequence 56, Application US/08469141A
; Patent No. 6124107
; GENERAL INFORMATION:
; APPLICANT: MUMFORD, RICHARD A.
; APPLICANT: DAVIES, D.T. PHILIP
; APPLICANT: DAHLGREN, MARY E.
; APPLICANT: BOGER, JOSHUA S.
; APPLICANT: HUMES, JOHN L.
; TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
; TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DR. CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000

; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,141A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 174611B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)-594-6734
; TELEFAX: (908)-594-4720
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-469-141A-56

Query Match 87.7%; Score 57; DB 3; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00089;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
| | | | |
Db 5 EGDFLAEGGGVR 16

RESULT 4

PCT-US95-13794-56
; Sequence 56, Application PC/TUS9513794
; GENERAL INFORMATION:
; APPLICANT: Mumford, Richard A.
; APPLICANT: Davies, D.T. Philip
; APPLICANT: Dahlgren, Mary E.
; APPLICANT: Boger, Joshua S.
; APPLICANT: Humes, John L.
; TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
; TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Christine E. Carty
; STREET: 126 E. Lincoln Avenue; P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13794
; FILING DATE: 03-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Carty, Christine E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 174611AY

TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
PCT-US95-13794-56

Query Match 87.7%; Score 57; DB 5; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00089;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGVR 13
| | | | | | | | | |
Db 5 EGDFLAEGGVR 16

RESULT 5
US-08-469-141A-46
; Sequence 46, Application US/08469141A
; Patent No. 6124107
; GENERAL INFORMATION:
; APPLICANT: MUMFORD, RICHARD A.
; APPLICANT: DAVIES, D.T. PHILIP
; APPLICANT: DAHLGREN, MARY E.
; APPLICANT: BOGER, JOSHUA S.
; APPLICANT: HUMES, JOHN L.
; TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
; POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DR. CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,141A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 174611B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)-594-6734
; TELEFAX: (908)-594-4720
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-469-141A-46

Query Match 87.7%; Score 57; DB 3; Length 17;

Best Local Similarity 91.7%; Pred. No. 0.00095;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGVR 13
| | | | | | | | | |
Db 1 EGDFLAEGGVR 12

RESULT 6
PCT-US95-13794-46
; Sequence 46, Application PC/TUS9513794
; GENERAL INFORMATION:
; APPLICANT: Mumford, Richard A.
; APPLICANT: Davies, D.T. Philip
; APPLICANT: Dahlgren, Mary E.
; APPLICANT: Boger, Joshua S.
; APPLICANT: Humes, John L.
; TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
; POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Christine E. Carty
; STREET: 126 E. Lincoln Avenue; P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13794
; FILING DATE: 03-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Carty, Christine E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 174611AY
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
PCT-US95-13794-46

Query Match 87.7%; Score 57; DB 5; Length 17;
Best Local Similarity 91.7%; Pred. No. 0.00095;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGVR 13
| | | | | | | | | |
Db 1 EGDFLAEGGVR 12

RESULT 7
US-08-469-141A-55
; Sequence 55, Application US/08469141A
; Patent No. 6124107
; GENERAL INFORMATION:
; APPLICANT: MUMFORD, RICHARD A.
; APPLICANT: DAVIES, D.T. PHILIP
; APPLICANT: DAHLGREN, MARY E.
; APPLICANT: BOGER, JOSHUA S.

```
; APPLICANT: HUMES, JOHN L.
; TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
; POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DR. CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,141A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 174611B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)-594-6734
; TELEFAX: (908)-594-4720
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; US-08-469-141A-55

Query Match      87.7%; Score 57; DB 3; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.001;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2  ESDFLAEGGGVR 13
    | | | | | | | | |
Db  5  EGDFLAEGGGVR 16

RESULT 8
PCT-US95-13794-55
; Sequence 55, Application PC/TUS9513794
; GENERAL INFORMATION:
; APPLICANT: Mumford, Richard A.
; APPLICANT: Davies, D.T. Philip
; APPLICANT: Dahlgren, Mary E.
; APPLICANT: Boger, Joshua S.
; APPLICANT: Humes, John L.
; TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
; POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Christine E. Carty
; STREET: 126 E. Lincoln Avenue, P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: PCT/US95/13794
; FILING DATE: 03-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Carty, Christine E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 174611AY
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; PCT-US95-13794-55

Query Match      87.7%; Score 57; DB 5; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.001;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2  ESDFLAEGGGVR 13
    | | | | | | | | |
Db  5  EGDFLAEGGGVR 16

RESULT 9
US-08-469-141A-54
; Sequence 54, Application US/08469141A
; Patent No. 6124107
; GENERAL INFORMATION:
; APPLICANT: MUMFORD, RICHARD A.
; APPLICANT: DAVIES, D.T. PHILIP
; APPLICANT: DAHLGREN, MARY E.
; APPLICANT: BOGER, JOSHUA S.
; APPLICANT: HUMES, JOHN L.
; TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
; POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DR. CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,141A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 174611B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)-594-6734
; TELEFAX: (908)-594-4720
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 US-08-469-141A-54

Query Match 87.7%; Score 57; DB 3; Length 19;
 Best Local Similarity 91.7%; Pred. No. 0.0011;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 10

PCT-US95-13794-54
 Sequence 54, Application PC/TUS9513794

GENERAL INFORMATION:

APPLICANT: Mumford, Richard A.
 APPLICANT: Davies, D.T. Philip
 APPLICANT: Dahlgren, Mary E.
 APPLICANT: Boger, Joshua S.
 APPLICANT: Humes, John L.
 TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
 POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
 NUMBER OF SEQUENCES: 71
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dr. Christine E. Carty
 STREET: 126 E. Lincoln Avenue, P.O. Box 2000
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/13794
 FILING DATE: 03-NOV-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
 NAME: Carty, Christine E.
 REGISTRATION NUMBER: 36,099
 REFERENCE/DOCKET NUMBER: 174611AY
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-6734

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 54:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

PCT-US95-13794-54

Query Match 87.7%; Score 57; DB 5; Length 19;
 Best Local Similarity 91.7%; Pred. No. 0.0011;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 11

US-08-288-657-1

Sequence 1, Application US/08288657
 Patent No. 5424291
 GENERAL INFORMATION:
 APPLICANT: Atrash, Butrus
 APPLICANT: Jones, David M.
 APPLICANT: Szelke, Michael
 TITLE OF INVENTION: New Isosteric Peptides
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Richard J. Sterner, Ph.D.
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/288,657
 FILING DATE:
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/751,700
 FILING DATE: 08-AUG-1991
 APPLICATION NUMBER: SE 9102462-0
 FILING DATE: 28-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Sterner Ph.D., Richard J.

REGISTRATION NUMBER: 35,372

REFERENCE/DOCKET NUMBER: 1103326-871

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-819-8783

TELEFAX: 212-354-8113

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..20

OTHER INFORMATION: /note= "Peptide sequence containing

thrombin cleavage site in the human fibrinogen

OTHER INFORMATION: A-alpha chain."

FEATURE:

NAME/KEY: Cleavage-site

LOCATION: 16..17

US-08-288-657-1

Query Match 87.7%; Score 57; DB 1; Length 20;
 Best Local Similarity 91.7%; Pred. No. 0.0011;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 12

US-07-984-884-1

Sequence 1, Application US/07984884

Patent No. 5614499

GENERAL INFORMATION:

APPLICANT: Teger-Nilsson, Ann-Catrine E

APPLICANT: Bylund, Ruth E

;; TITLE OF INVENTION: New peptide derivatives
;; NUMBER OF SEQUENCES: 1
;; CORRESPONDENCE ADDRESS:
;; APPLICANT: White and Case
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: United States
;; ZIP: 10036-2787
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/984,884
;; FILING DATE: 02-DEC-1992
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sterner, Richard J
;; REGISTRATION NUMBER: 35, 372
;; REFERENCE/DOCKET NUMBER: 1103326-016
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)819-8200
;; TELEFAX: (212)354-8113
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
US-07-984-884-1

Query Match 87.7%; Score 57; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 13
US-08-481-810-1
;; Sequence 1, Application US/08481810
;; Patent No. 5736521
;; GENERAL INFORMATION:
;; APPLICANT: Teger-Nilsson, Ann-Catrine E
;; APPLICANT: Bylund, Ruth E
;; TITLE OF INVENTION: New peptide derivatives
;; NUMBER OF SEQUENCES: 1
;; CORRESPONDENCE ADDRESS:
;; APPLICANT: White and Case
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: United States
;; ZIP: 10036-2787
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/481,810
;; FILING DATE:
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/984884
;; FILING DATE: 02-DEC-1992
;; CLASSIFICATION: 514

;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sterner, Richard J
;; REGISTRATION NUMBER: 35,372
;; REFERENCE/DOCKET NUMBER: 1103326-016
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)819-8200
;; TELEFAX: (212)354-8113
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
US-08-481-810-1

Query Match 87.7%; Score 57; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 14
US-08-484-426-1
;; Sequence 1, Application US/08484426
;; Patent No. 5747460
;; GENERAL INFORMATION:
;; APPLICANT: Teger-Nilsson, Ann-Catrine E
;; APPLICANT: Bylund, Ruth E
;; TITLE OF INVENTION: New peptide derivatives
;; NUMBER OF SEQUENCES: 1
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: White and Case
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: United States
;; ZIP: 10036-2787
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/484,426
;; FILING DATE:
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/984884
;; FILING DATE: 02-DEC-1992
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sterner, Richard J
;; REGISTRATION NUMBER: 35,372
;; REFERENCE/DOCKET NUMBER: 1103326-016
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)819-8200
;; TELEFAX: (212)354-8113
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
US-08-484-426-1

Query Match 87.7%; Score 57; DB 1; Length 20;

Best Local Similarity 91.7%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
| | | | | | | | | |
Db 5 EGDFLAEGGGVR 16

RESULT 15

US-08-480-818-1
; Sequence 1, Application US/08480818
; Patent No. 5955433
; GENERAL INFORMATION:
; APPLICANT: Teger-Nilsson, Ann-Catrine E
; APPLICANT: Bylund, Ruth E
; TITLE OF INVENTION: New peptide derivatives
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,818
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/984884
; FILING DATE: 02-DEC-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)819-8200
; TELEFAX: (212)354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-480-818-1

Query Match 87.7%; Score 57; DB 2; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
| | | | | | | | | |
Db 5 EGDFLAEGGGVR 16

Search completed: February 10, 2003, 16:07:45
Job time : 16 secs

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OM protein - protein search, using sw model

Run on: February 10, 2003, 16:02:52 ; Search time 29 Seconds
(without alignments)
11.453 Million cell updates/sec

Title: US-09-845-729-1

Perfect score: 65

Sequence: 1 SESDFLAEGGVR 13

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 140259 seqs, 25548876 residues

Total number of hits satisfying chosen parameters: 140259

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
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3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	87.7	12	9	US-09-845-725-1
2	57	87.7	15	9	US-09-845-719A-1
3	57	87.7	16	9	US-09-846-780-1
4	57	87.7	16	9	US-09-826-290-352
5	57	87.7	25	9	US-09-757-774-16
6	57	87.7	360	10	US-09-925-297-587
7	57	87.7	847	9	US-10-112-527-4
8	52	80.0	10	9	US-09-846-350-1
9	52	80.0	11	9	US-09-846-342-1
10	46	70.8	17	9	US-10-057-505-11
11	42	64.6	98	10	US-09-740-668A-18
12	39	60.0	1164	10	US-09-834-792-5
13	39	60.0	1165	9	US-10-026-188-8
14	39	60.0	2039	9	US-10-192-584-7
15	38	58.5	154	10	US-09-925-300-1763
16	36	55.4	359	9	US-09-972-758-2
17	36	55.4	359	10	US-09-745-763-34
18	36	55.4	426	10	US-09-864-761-42921
19	35.5	54.6	418	9	US-09-738-626-5679

20	35	53.8	621	10	US-09-815-242-11303	Sequence 11303, A
21	35	53.8	845	9	US-09-738-626-4347	Sequence 4347, Ap
22	35	53.8	2042	9	US-10-192-584-6	Sequence 6, Appli
23	34	52.3	37	10	US-09-813-345-7	Sequence 7, Appli
24	34	52.3	192	9	US-09-738-626-5432	Sequence 5432, Ap
25	34	52.3	211	10	US-09-925-302-467	Sequence 467, App
26	34	52.3	272	9	US-09-774-639-167	Sequence 167, App
27	34	52.3	487	10	US-09-841-132-349	Sequence 349, App
28	34	52.3	583	10	US-09-841-132-353	Sequence 353, App
29	34	52.3	821	10	US-09-841-132-195	Sequence 195, App
30	34	52.3	1294	10	US-09-815-242-13724	Sequence 13724, A
31	34	52.3	1770	10	US-09-841-132-444	Sequence 444, App
32	34	52.3	1776	10	US-09-841-132-179	Sequence 179, App
33	33	50.8	36	8	US-08-424-5508-579	Sequence 579, App
34	33	50.8	263	10	US-09-815-242-11707	Sequence 11707, A
35	33	50.8	293	10	US-09-861-205-2	Sequence 2, Appli
36	33	50.8	293	12	US-10-054-313-2	Sequence 2, Appli
37	33	50.8	304	9	US-09-738-626-3928	Sequence 3928, Ap
38	33	50.8	314	9	US-09-738-626-6390	Sequence 6390, Ap
39	33	50.8	355	10	US-09-815-242-11457	Sequence 11457, A
40	33	50.8	355	10	US-09-815-242-11620	Sequence 11620, A
41	33	50.8	424	9	US-09-843-905A-13	Sequence 13, Appli
42	33	50.8	479	10	US-09-925-300-1515	Sequence 1515, Ap
43	33	50.8	640	9	US-09-983-204-16	Sequence 16, Appli
44	33	50.8	696	10	US-09-809-790-2	Sequence 2, Appli
45	33	50.8	696	10	US-09-809-617-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-845-725-1

; Sequence 1, Application US/09845725

; Patent No. US20020161185A1

; GENERAL INFORMATION:

; APPLICANT: Jackowski, George

; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR

; FILE REFERENCE: 2132.028

; CURRENT APPLICATION NUMBER: US/09/845,725

; CURRENT FILING DATE: 2001-04-30

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-845-725-1

Query Match 87.7%; Score 57; DB 9; Length 12;

Best Local Similarity 91.7%; Pred. No. 0.0012;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGVR 13

Db 1 EGDFLAEGGVR 12

RESULT 2

US-09-845-719A-1

; Sequence 1, Application US/09845719A

; Patent No. US20020161179A1

; GENERAL INFORMATION:

; APPLICANT: Jackowski, George

; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR

; FILE REFERENCE: 2132.035

; CURRENT APPLICATION NUMBER: US/09/845,719A

; CURRENT FILING DATE: 2001-04-30

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

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; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-719A-1

Query Match      87.7%; Score 57; DB 9; Length 15;
Best Local Similarity 91.7%; Pred. No. 0.0015;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 4 EGDFLAEGGGVR 15

RESULT 3
US-09-846-780-1
; Sequence 1, Application US/09846780
; Patent No. US20020160423A1
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; FILE REFERENCE: 2132.039
; CURRENT APPLICATION NUMBER: US/09/846,780
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-846-780-1

Query Match      87.7%; Score 57; DB 9; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.0016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 4
US-09-826-290-352
; Sequence 352, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 352
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; LENGTH: 16
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-352

Query Match      87.7%; Score 57; DB 9; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.0016;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 5
US-09-757-774-16
; Sequence 16, Application US/09757774
; Publication No. US20020187156A1
; GENERAL INFORMATION:
; APPLICANT: Dintzis, Howard M.
; APPLICANT: Dintzis, Renee
; APPLICANT: Blodgett, James
; APPLICANT: Cheronis, John
; TITLE OF INVENTION: THERAPEUTIC SUPPRESSION OF SPECIFIC IMMUNE RESPONSES BY
; TITLE OF INVENTION: ADMINISTRATION OF OLIGOMERIC FORMS OF ANTIGEN OF CONTROLLED
; FILE REFERENCE: 07265/124004
; CURRENT APPLICATION NUMBER: US/09/757,774
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 08/440,322
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: US 07/808,797
; PRIOR FILING DATE: 1991-12-17
; PRIOR APPLICATION NUMBER: US 07/628,858
; PRIOR FILING DATE: 1990-12-17
; PRIOR APPLICATION NUMBER: US 07/354,710
; PRIOR FILING DATE: 1989-05-22
; PRIOR APPLICATION NUMBER: US 07/248,293
; PRIOR FILING DATE: 1988-09-21
; PRIOR APPLICATION NUMBER: US 06/869,808
; PRIOR FILING DATE: 1986-05-29
; PRIOR APPLICATION NUMBER: US 06/460,266
; PRIOR FILING DATE: 1983-01-24
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(25)
; OTHER INFORMATION: Xaa = O-ACA/Pro
US-09-757-774-16

Query Match      87.7%; Score 57; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.0025;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 7 EGDFLAEGGGVR 18

RESULT 6
US-09-925-297-587
; Sequence 587, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
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US-09-845-729-1

Query Match 87.7%; Score 57; DB 10; Length 360;
Best Local Similarity 91.7%; Pred. No. 0.036;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 45 EGDFLAEGGGVR 56

RESULT 7

US-10-112-527-4

Sequence 4, Application US/10112527
Patent No. US20020168722A1
GENERAL INFORMATION:
APPLICANT: Grieninger, Gerd
APPLICANT: Aplegate, Dianne
APPLICANT: Stoike-Steben, Lara
TITLE OF INVENTION: NO. US20020168722A1el Cleaved Fragments of Fibrinogen
FILE REFERENCE: Docket 454-24 CON
CURRENT APPLICATION NUMBER: US/10/112,527
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: US 09/373,157
PRIOR FILING DATE: 1999-08-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 847
TYPE: PRT
ORGANISM: Homo sapiens

US-10-112-527-4

Query Match 87.7%; Score 57; DB 9; Length 847;
Best Local Similarity 91.7%; Pred. No. 0.086;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 8

US-09-846-350-1

Sequence 1, Application US/09846350
Patent No. US20020161188A1
GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: Biopolymer Marker Indicative of Disease State Having a Molecular
FILE REFERENCE: 2132.025
CURRENT APPLICATION NUMBER: US/09/846,350
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens

US-09-846-350-1

Query Match 80.0%; Score 52; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DFLAEGGGVR 13
Db 1 DFLAEGGGVR 10

RESULT 9

US-09-846-342-1

Sequence 1, Application US/09846342
Patent No. US20020160422A1
GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
FILE REFERENCE: 2132.026
CURRENT APPLICATION NUMBER: US/09/846,342
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens

US-09-846-342-1

Query Match 80.0%; Score 52; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DFLAEGGGVR 13
Db 2 DFLAEGGGVR 11

RESULT 10

US-10-057-505-11

Sequence 11, Application US/10057505
Patent No. US20020164674A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: AURORA BIOSCIENCES CORPORATION
APPLICANT: TSJEN, Roger
APPLICANT: HEIM, Roger
APPLICANT: CUBITT, Andrew
TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
FILE REFERENCE: REGEN1260-3
CURRENT APPLICATION NUMBER: US/10/057,505
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 08/792,553
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: US 09/396,003
PRIOR FILING DATE: 1999-09-13

US-09-846-350-1

Sequence 1, Application US/09846350
Patent No. US20020161188A1
GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: Biopolymer Marker Indicative of Disease State Having a Molecular
FILE REFERENCE: 2132.025
CURRENT APPLICATION NUMBER: US/09/846,350
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens

US-09-846-350-1

Query Match 80.0%; Score 52; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DFLAEGGGVR 13
Db 1 DFLAEGGGVR 10

RESULT 9

US-09-846-342-1

Sequence 1, Application US/09846342
Patent No. US20020160422A1
GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
FILE REFERENCE: 2132.026
CURRENT APPLICATION NUMBER: US/09/846,342
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens

US-09-846-342-1

Query Match 80.0%; Score 52; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DFLAEGGGVR 13
Db 2 DFLAEGGGVR 11

RESULT 10

US-10-057-505-11

Sequence 11, Application US/10057505
Patent No. US20020164674A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: AURORA BIOSCIENCES CORPORATION
APPLICANT: TSJEN, Roger
APPLICANT: HEIM, Roger
APPLICANT: CUBITT, Andrew
TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
FILE REFERENCE: REGEN1260-3
CURRENT APPLICATION NUMBER: US/10/057,505
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 08/792,553
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: US 09/396,003
PRIOR FILING DATE: 1999-09-13

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; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Linker moiety
US-10-057-505-11

Query Match          70.8%; Score 46; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  5 FLAEGGGVR 13
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Db  1 FLAEGGGVR 9

RESULT 11
US-09-740-668A-18
; Sequence 18, Application US/09740668A
; Patent No. US20020076700A1
; GENERAL INFORMATION:
; APPLICANT: Shinketsu, Richard
; TITLE OF INVENTION: NO. US20020076700A1el polypeptides and nucleic acids encoding sam
; FILE REFERENCE: 15966-537 CIP
; CURRENT APPLICATION NUMBER: US/09/740,668A
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: PCT/US99/29584
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/465,512
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/113,485
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/112,837
; PRIOR FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-668A-18

Query Match          64.6%; Score 42; DB 10; Length 98;
Best Local Similarity 63.6%; Pred. No. 2.7;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy  3 SDFLAEGGGVR 13
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Db  50 ADFLGGGGVQ 60

RESULT 12
US-09-834-792-5
; Sequence 5, Application US/09834792
; Patent No. US20020037515A1
; GENERAL INFORMATION:
; APPLICANT: Mount Sinai School of Medicine of NYU
; TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL
; FILE REFERENCE: CHANNEL EXPRESSED IN TASTE RECEPTOR CELL
; FILE REFERENCE: AP32911 070165.0589
; CURRENT APPLICATION NUMBER: US/09/834,792
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,491
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1164
; TYPE: PRT
; ORGANISM: Human

US-09-834-792-5
Query Match          60.0%; Score 39; DB 10; Length 1164;
Best Local Similarity 61.5%; Pred. No. 1e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy  1 SESDFLAEGGGVR 13
    |||||
Db  1117 SVADVLQAQGGPR 1129

RESULT 13
US-10-026-188-8
; Sequence 8, Application US/10026188
; Patent No. US20020164645A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; TITLE OF INVENTION: Ion Channel
; FILE REFERENCE: 02307E-114910US
; CURRENT APPLICATION NUMBER: US/10/026,188
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/259,379
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 1165
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human ltrpc6
US-10-026-188-8

Query Match          60.0%; Score 39; DB 9; Length 1165;
Best Local Similarity 61.5%; Pred. No. 1e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy  1 SESDFLAEGGGVR 13
    |||||
Db  1118 SVADVLQAQGGPR 1130

RESULT 14
US-10-192-584-7
; Sequence 7, Application US/10192584
; Publication No. US20030027987A1
; GENERAL INFORMATION:
; APPLICANT: TOKUNAGA, Eiji
; APPLICANT: SAKAGUCHI, Masashi
; MATSUO, Kazuo
; HAMADA, Fukusaburo
; TOKIYOSHI, Sachio
; TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS
; PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 624 Ninth Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/192,584
; FILING DATE: 11-Jul-2002
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,098
; FILING DATE: 19-May-1998
; APPLICATION NUMBER: PCT/JP97/03222
; FILING DATE: 12-SEP-1997
; APPLICATION NUMBER: JP 27,148/1996
; FILING DATE: 19-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: KORNBAU, Anne M.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TOKUNAGA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2039 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-192-584-7

Query Match          60.0%; Score 39; DB 9; Length 2039;
Best Local Similarity 61.5%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SESDFLAEGGVV 13
Db 786 SEIDLLQGGVQ 798
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RESULT 15
US-09-925-300-1763
; Sequence 1763, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1763
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1763
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Query Match          58.5%; Score 38; DB 10; Length 154;
Best Local Similarity 72.7%; Pred. NO. 19;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SESDFLAEGGG 11
Db 28 SLTDFLAEDGG 38
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Job time : 29 secs

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OM protein - protein search, using sw model

Run on: February 10, 2003, 15:58:46 ; Search time 16 Seconds
(without alignments)
78.109 Million cell updates/sec

Title: US-09-845-729-1

Perfect score: 65

Sequence: 1 SESDFLAEGGVR 13

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	93.8	16	2 H29501	fibrinopeptide A -
2	57	87.7	16	2 C28854	fibrinopeptide A -
3	57	87.7	16	2 A24180	fibrinogen alpha C
4	57	87.7	16	2 B24180	fibrinogen alpha C
5	57	87.7	16	2 A28854	fibrinopeptide A -
6	57	87.7	16	2 B28854	fibrinopeptide A -
7	57	87.7	16	2 A29501	fibrinopeptide A -
8	57	87.7	644	1 FGHUA	fibrinogen alpha C
9	57	87.7	866	2 D44234	fibrinogen alpha C
10	52	80.0	15	2 F29501	fibrinopeptide A -
11	51	78.5	16	2 G29501	fibrinopeptide A -
12	51	78.5	28	2 A05296	fibrinogen alpha C
13	49	75.4	17	2 E29501	fibrinopeptide A -
14	48	73.8	15	2 I29501	fibrinopeptide A -
15	48	73.8	19	2 B29501	fibrinopeptide A -
16	48	73.8	19	2 C29501	fibrinopeptide A -
17	48	73.8	311	2 A05294	fibrinogen alpha C
18	40	61.5	15	2 F0101	fibrinogen alpha C
19	40	61.5	280	2 H9800	hypothetical prote
20	39	60.0	236	2 S48867	dimethylallyltrans
21	39	60.0	245	2 AG0701	Orf 245 protein [i
22	39	60.0	271	2 S18730	aminoglycoside N3
23	39	60.0	324	2 D70943	hypothetical prote
24	39	60.0	705	2 T31157	hypothetical prote
25	38.5	59.2	732	2 AB2732	conserved hypothet
26	38.5	59.2	741	2 B97513	probable secreted
27	38	58.5	575	2 T48224	probable homeodoma
28	38	58.5	611	1 S12566	translation initia
29	38	58.5	652	2 AD2316	hypothetical prote

ALIGNMENTS

RESULT 1

H29501

fibrinopeptide A - gray seal

C:Species: Halichoerus grypus (gray seal)

C:Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000

C:Accession: H29501

R:Blombaeck, B.; Blombaeck, M.; Hann, C.

unpublished results, cited by Blombaeck, M., in Chemotaxonomy and Ser

A:Reference number: A29501

A:Accession: H29501

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <BLO>

C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 93.8%; Score 61; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGVR 13

Db 5 ESDFLAEGGVR 16

RESULT 2

C28854

fibrinopeptide A - gelada baboon

C:Species: Theropithecus gelada (gelada baboon)

C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996

C:Accession: C28854

R:Nakamura, S.; Takenaka, O.; Takahashi, K.

J. Biochem. 94, 1973-1978, 1983

A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit

A:Reference number: A91973; MUID:84161822; PMID:6423621

A:Accession: C28854

A:Molecule type: protein

A:Residues: 1-16 <NAK>

C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;

Best Local Similarity 91.7%; Pred. No. 0.00076;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGVR 13

Db 5 EGDFLAEGGVR 16

RESULT 3

A24180

fibrinogen alpha chain - Japanese macaque (fragment)

N:Contains: fibrinopeptide A

C:Species: Macaca fuscata (Japanese macaque)
 C>Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 26-Jan-1996
 C:Accession: A24180
 R:Nakamura, S.; Takenaka, O.; Takahashi, K.
 J. Biochem. 97, 1487-1492, 1985
 A:Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E. venosa), and baboons.
 A:Reference number: A91990; MUID:85289140; PMID:3928610
 A:Accession: A24180
 A:Molecule type: protein
 A:Residues: 1-16 <NAK>
 C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.00076;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 4
 B24180
 fibrinogen alpha chain - red guenon (fragment)
 N:Contains: fibrinopeptide A
 C:Species: Erythrocebus patas (red guenon, hussar)
 C>Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
 C:Accession: B24180
 R:Nakamura, S.; Takenaka, O.; Takahashi, K.
 J. Biochem. 97, 1487-1492, 1985
 A:Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E. venosa), and baboons.
 A:Reference number: A91990; MUID:85289140; PMID:3928610
 A:Accession: B24180
 A:Molecule type: protein
 A:Residues: 1-16 <NAK>
 C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.00076;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 5
 A28854
 fibrinopeptide A - olive baboon
 C:Species: Papio anubis, Papio hamadryas anubis (olive baboon)
 C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
 C:Accession: A28854
 R:Nakamura, S.; Takenaka, O.; Takahashi, K.
 J. Biochem. 94, 1973-1978, 1983
 A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus aethiopicus)
 A:Reference number: A91973; MUID:84161822; PMID:6423621
 A:Accession: A28854
 A:Molecule type: protein
 A:Residues: 1-16 <NAK>
 C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.00076;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 6
 A28854
 fibrinopeptide A - olive baboon
 C:Species: Papio anubis, Papio hamadryas anubis (olive baboon)
 C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
 C:Accession: A28854
 R:Nakamura, S.; Takenaka, O.; Takahashi, K.
 J. Biochem. 94, 1973-1978, 1983
 A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus aethiopicus)
 A:Reference number: A91973; MUID:84161822; PMID:6423621
 A:Accession: A28854
 A:Molecule type: protein
 A:Residues: 1-16 <NAK>
 C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.00076;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 6

B28854
 fibrinopeptide A - hamadryas baboon
 C:Species: Papio hamadryas (hamadryas baboon)
 C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
 C:Accession: B28854
 R:Nakamura, S.; Takenaka, O.; Takahashi, K.
 J. Biochem. 94, 1973-1978, 1983
 A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus aethiopicus)
 A:Reference number: A91973; MUID:84161822; PMID:6423621
 A:Accession: B28854
 A:Molecule type: protein
 A:Residues: 1-16 <NAK>
 C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.00076;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 7
 A29501
 fibrinopeptide A - baboon
 C:Species: Papio sp. (baboon)
 C>Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 26-Jan-1996
 C:Accession: A29501
 R:Blombaeck, B.; Blombaeck, M.; Hann, C.
 unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Serology of Baboons
 A:Reference number: A29501
 A:Accession: A29501
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-16 <BLO>
 C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
 Best Local Similarity 91.7%; Pred. No. 0.00076;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGDFLAEGGGVR 16

RESULT 8
 FGHUA
 fibrinogen alpha chain precursor, short splice form [validated] - human
 N:Alternate names: coagulation factor I
 N:Contains: fibrinopeptide A
 C:Species: Homo sapiens (man)
 C>Date: 24-Apr-1984 #sequence_revision 30-Jun-1987 #text_change 08-Dec-2000
 C:Accession: A93956; A43568; I84456; I84456; A44234; C44234; B94433; A90433; B94309; S19
 R:Kant, J.A.; Lord, S.T.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
 A:Title: Partial mRNA sequences for human Aalpha, Bbeta, and gamma fibrinogen chains: evolution and expression
 A:Reference number: A93956; MUID:83247396; PMID:6575389
 A:Accession: A93956
 A:Molecule type: mRNA
 A:Residues: 1-644 <KAN>
 A:Cross-references: GB:J00128; NID:G182425; PIDN:AAA52427.1; PID:G182426
 A:Note: the authors translated the codon GAG for residue 247 as Gly, GGA for residue 438
 R:Chung, D.W.; Harris, J.E.; Davie, E.W.
 Adv. Exp. Med. Biol. 281, 39-48, 1990
 A:Title: Nucleotide sequences of the three genes coding for human fibrinogen.
 A:Reference number: A43568; MUID:91344740; PMID:2102623
 A:Accession: A43568
 A:Molecule type: DNA
 A:Residues: 1-330, A, 332-644 <CHU>
 A:Cross-references: GB:M64982; NID:G458553; PIDN:AAA17055.1; PID:G458554
 R:Rixon, M.W.; Chan, W.Y.; Davie, E.W.; Chung, D.W.

Biochemistry 22, 3237-3244, 1983
A>Title: Characterization of a complementary deoxyribonucleic acid coding for the alpha
A;Reference number: A90468; MUID:83283432; PMID:6688355
A;Accession: A90468
A;Molecule type: mRNA
A;Residues: 1-330,'A',332-629 <R1X>
A;Cross-references: GB:J00127; NID:g182423; PIDN:AAA52426.1; PID:g182424
R;Imam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1983
A>Title: Isolation and characterization of cDNA clones for the Aalpha- and gamma-chains
A;Reference number: I37393; MUID:84069777; PMID:6689067
A;Accession: I84456
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 110-156 <RES>
A;Cross-references: GB:K02272; NID:g182427; PIDN:AAA52428.1; PID:g182428
R;Fu, Y.; Weisbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma
Biochemistry 31, 11968-11972, 1992
A>Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel
A;Reference number: A44234; MUID:93090725; PMID:1457396
A;Accession: A44234
A;Molecule type: mRNA
A;Residues: 1-51 <FUI>
A;Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554
A;Note: sequence extracted from NCBI backbone (NCBIN:119912, NCBIN:119914, NCBIP:119918)
A;Accession: C44234
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 605-644 <FUI>
A;Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554
A;Note: sequence extracted from NCBI backbone (NCBIN:119920)
R;Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
in Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, Pe
A>Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v
A;Reference number: A94433
A;Accession: B94433
A;Molecule type: protein
A;Residues: 20-214,'RS',217-298,'G',300-303,'G',305-629 <HEN>
R;Watt, K.W.K.; Cottrell, B.A.; Strong, D.D.; Doolittle, R.F.
Biochemistry 18, 5410-5416, 1979
A>Title: Amino acid sequence studies on the alpha chain of human fibrinogen. Overlappi
A;Reference number: A90433; MUID:8008231; PMID:518846
A;Contents: disulfide bonds
A;Accession: A90433
A;Molecule type: protein
A;Residues: 20-146,'Q',148-195,'N',197-230,'N',232-316,'SG',319-406,'D',408,'N',410-629
R;Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
A>Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A;Reference number: A94309; MUID:76225080; PMID:936108
A;Contents: variant, and disulfide bonds
A;Accession: B94309
A;Molecule type: protein
A;Residues: 20-65,'T',67-629 <BLO>
R;Dewey, R.S.; Liesch, J.M.; Williams, H.R.; Sugg, E.E.; Dolan, C.A.; Davies, P.; Mumfo
Biochem. J. 281, 519-524, 1992
A>Title: Purification and characterization by fast-atom-bombardment mass spectrometry of
incubation with calcium ionophore A23187.
A;Reference number: S19297; MUID:92143822; PMID:1736899
A;Accession: S19297
A;Molecule type: protein
A;Residues: 20-40 <DEW>
R;Retzius, A.D.; Markland Jr., F.S.
Thromb. Res. 52, 541-552, 1988
A>Title: A direct-acting fibrinolytic enzyme from the venom of Agkistrodon contortrix co
A;Reference number: A60905; MUID:89162316; PMID:3232124
A;Accession: A60905
A;Molecule type: protein
A;Residues: 433-451 <RET>
R;Fretto, L.J.; Ferguson, E.W.; Steinman, H.M.; McKee, P.A.
J. Biol. Chem. 253, 2184-2195, 1978
A>Title: Localization of the alpha-chain cross-link acceptor sites of human fibrin.
A;Reference number: A92225; MUID:78130085; PMID:632262

A;Contents: annotation; cross-linking acceptor sites
R;Cottrell, B.A.; Strong, D.D.; Watt, K.W.K.; Doolittle, R.F.
Biochemistry 18, 5405-5410, 1979
A>Title: Amino acid sequence studies on the alpha chain of human fibrinogen. Exact locat
A;Reference number: A90432; MUID:8008230; PMID:518845
A;Contents: annotation; cross-linking acceptor sites
R;Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A>Title: Covalent structure of fibrinogen.
A;Reference number: A90037; MUID:83254370; PMID:6575689
A;Contents: annotation; review, disulfide bonds
R;Itarte, E.; Plana, M.; Guasch, M.D.; Martos, C.
Biochem. Biophys. Res. Commun. 117, 631-636, 1983
A>Title: Phosphorylation of fibrinogen by casein kinase 1.
A;Reference number: A90116; MUID:84104274; PMID:6318767
A;Contents: annotation; phosphorylation
A;Note: about one-third of alpha chain molecules in blood were found to be phosphorylate
R;Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A>Title: Fibrinogen and fibrin.
A;Reference number: A90041; MUID:84305751; PMID:6383194
A;Contents: annotation; review, EM structure, polymerization, ligands
R;Kimura, S.; Aoki, N.
J. Biol. Chem. 261, 15591-15595, 1986
A>Title: Cross-linking site in fibrinogen for alpha-2-plasmin inhibitor.
A;Reference number: A92565; MUID:87057190; PMID:2877981
A;Contents: annotation; cross-linking site for alpha-2-plasmin inhibitor
R;Kishnamurthi, S.; Dickens, T.A.; Patel, Y.; Wheeler-Jones, C.P.D.; Kakkar, V.V.
Biochem. Biophys. Res. Commun. 163, 1256-1264, 1989
A>Title: The fibrinogen-derived peptide (RGDS) prevents proteolytic degradation of prote
A;Reference number: A33261; MUID:89392031; PMID:2783136
A;Contents: annotation; activity of cell attachment (R-G-D) motif
R;Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A>Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-te
A;Reference number: A37117; MUID:90337977; PMID:2143188
A;Contents: annotation; hementin cleavage site
A;Note: hementin, a protease from Haemeteria ghiliani, the giant South American leech,
R;Staedker, L.; Sillard, R.; Bensch, K.W.; Ruf, A.; Raida, M.; Schulz-Knappe, P.; Schep
Biochem. Biophys. Res. Commun. 215, 896-902, 1995
A>Title: In vivo degradation of human fibrinogen A alpha: Detection of cleavage sites an
A;Reference number: JC4334; MUID:96027996; PMID:7498058
A;Contents: annotation; composition and amino-terminal sequences of carboxyl end peptide
C;Comment: Unlike the beta and gamma chains, the alpha chain is not glycosylated.
C;Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibrinectin.
C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
ization sites responsible for the formation of the soft clot
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
ger) and between alpha chains (weaker) of different monomers.
C;Comment: All fibrinogen chains are synthesized in the liver.
C;Comment: See PIR:D44234 for the minor alternative splice form.
C;Genetics:
A;Gene: GDB:FGA
A;Cross-references: GDB:119129; OMM:134820
A;Map position: 4q28-4q28
A;Introns: 18/3; 122/1; 171/2
A;Note: the list of introns is incomplete
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha, beta (see
ins are contained in the core. Two three-chain coiled coils emerge from this core and co
from the distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A;Pathway: blood coagulation
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
C;Keywords: alternative splicing; blood coagulation; coiled coil; glycoprotein; liver; pi
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-629/Product: fibrinogen alpha chain #status experimental <APT>
F;20-35/Product: fibrinopeptide A #status experimental <P>
F;36-629/Product: fibrin alpha chain #status experimental <PGA>
F;36-38/Region: polymerization site, binding to the distal domain of the gamma chain of
F;57-185/Domain: fibrinogen disulfide ring homology <FDR>
F;591-593/Region: cell attachment (R-G-D) motif
F;22,460/Binding site: phosphate (Ser) (covalent) #status experimental

F:35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
 F:47/Disulfide bonds: interchain (to alpha-47) #status experimental
 F:55/Disulfide bonds: interchain (to beta-95) #status experimental
 F:64/Disulfide bonds: interchain (to gamma-49) #status experimental
 F:68/Disulfide bonds: interchain (to beta-106) #status experimental
 F:180/Disulfide bonds: interchain (to gamma-165) #status experimental
 F:184/Disulfide bonds: interchain (to beta-223) #status experimental
 F:288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
 F:322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
 F:347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
 F:461-491/Disulfide bonds: #status experimental
 F:527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status
 Query Match 87.7%; Score 57; DB 1; Length 644;
 Best Local Similarity 91.7%; Pred. No. 0.039;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 24 EGDFLAEGGGVR 35
 | | | | | | | | | |
 RESULT 9
 D44234
 fibrinogen alpha chain precursor, extended splice form - human
 N:Alternate names: coagulation factor I
 N:Contains: fibrinopeptide A
 C:Species: Homo sapiens (man)
 C:Date: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 19-Jan-2001
 C:Accession: D44234; B44234
 R:Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma
 Biochemistry 31, 11968-11972, 1992
 A:Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a nove
 A:Reference number: A44234; PMID:93090725; PMID:1457396
 A:Accession: D44234
 A:Status: translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA; DNA
 A:Residues: 1-866 <FU1>
 A:Cross-references: GB:M59569; NID:g182406; PID:g182407
 A:Note: neither the complete nucleic acid sequence nor the complete translation are show
 A:Accession: B44234
 A:Molecule type: mRNA; DNA
 A:Residues: 605-866 <FU2>
 A:Note: sequence extracted from NCBI backbone (NCBI:119917)
 C:Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibrinectin.
 C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
 ation sites responsible for the formation of the soft clot.
 C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
 ger) and between alpha chains (weaker) of different monomers.
 C:Comment: All fibrinogen chains are synthesized in the liver.
 C:Comment: See PIR:FGHUA for the major splice form. It is not known whether this form is
 C:Genetics:
 A:Gene: GDB:FGA
 A:Cross-references: GDB:119129; OMIM:134820
 A:Map position: 4q28-4q28
 A:Introns: 18/3; 60/3; 122/1; 171/2
 A:Note: the list of introns is incomplete
 C:Complex: the fibrinogen molecule is a hexamer containing two sets of three nonidentica
 nained in the core. two three-chain coiled coils emerge from this core and connect it t
 distal domain nodes.
 C:Function:
 A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
 A:Pathway: blood coagulation
 C:Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma
 C:Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <MAT>
 F:20-35/Product: fibrinopeptide A #status experimental <APT>
 F:36-863/Product: fibrin alpha chain, extended splice form #status predicted <FGA>
 F:57-185/Domain: fibrinogen disulfide ring homology <FDR>
 F:591-593/Region: cell attachment (R-G-D) motif
 F:629-863/Domain: fibrinogen beta/gamma homology <FBG>
 F:42,460/Binding site: phosphate (Ser) (covalent) #status experimental

F:35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
 F:47/Disulfide bonds: interchain (to alpha-47) #status experimental
 F:55/Disulfide bonds: interchain (to beta-95) #status experimental
 F:64/Disulfide bonds: interchain (to gamma-49) #status experimental
 F:68/Disulfide bonds: interchain (to beta-106) #status experimental
 F:180/Disulfide bonds: interchain (to gamma-165) #status experimental
 F:184/Disulfide bonds: interchain (to beta-223) #status experimental
 F:288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
 F:322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
 F:347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
 F:461-491/Disulfide bonds: #status experimental
 F:527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status
 F:686,831/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 87.7%; Score 57; DB 2; Length 866;
 Best Local Similarity 91.7%; Pred. No. 0.053;
 Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 0;
 QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 24 EGDFLAEGGGVR 35
 | | | | | | | | | |
 RESULT 10
 F29501
 fibrinopeptide A - wombat
 C:Species: Vombatidae gen. sp. (wombat)
 C:Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
 C:Accession: F29501
 R:Blombaeck, B.; Blombaeck, M.; Hann, C.
 unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
 A:Reference number: A29501
 A:Accession: F29501
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <BLO>
 C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
 Query Match 80.0%; Score 52; DB 2; Length 15;
 Best Local Similarity 76.9%; Pred. No. 0.0056;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 SESDFLAEGGGVR 13
 : | | | | | | | | | |
 Db 3 TEGSFLAEGGGVR 15
 | | | | | | | | | |
 RESULT 11
 G29501
 fibrinopeptide A - bear
 C:Species: Ursus sp. (bear)
 C:Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
 C:Accession: G29501
 R:Blombaeck, B.; Blombaeck, M.; Hann, C.
 unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
 A:Reference number: A29501
 A:Accession: G29501
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-16 <BLO>
 C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf
 Query Match 78.5%; Score 51; DB 2; Length 16;
 Best Local Similarity 75.0%; Pred. No. 0.009;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ESDFLAEGGGVR 13
 | | | | | | | | | |
 Db 5 EGEFLAEGGGVR 16
 | | | | | | | | | |
 RESULT 12
 A05296

fibrinogen alpha chain - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 25-Oct-1996
C:Accession: A94308; A03118; A05296; B37511; C03118
R:Birken, S.; Wilner, G.D.; Canfield, R.E.
Thromb. Res. 7, 599-610, 1975
A:Title: Studies of the structure of canine fibrinogen.
A:Reference number: A94308; MUID:76081726; PMID:1198547
A:Accession: A94308
A:Molecule type: protein
A:Residues: 1-28 <BIR>
R:Blombaek, B.; Blombaek, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A:Title: Studies on fibrinopeptides from mammals.
A:Reference number: A03118
A:Accession: A03118
A:Molecule type: protein
A:Residues: 1-16 <BLO>
R:Oebahr Jr., A.J.; Colman, R.W.; Laki, K.; Gladner, J.A.
Biochem. Biophys. Res. Commun. 14, 555-558, 1964
A:Reference number: A37511; MUID:66020594; PMID:5836555
A:Accession: A37511
A:Molecule type: protein
A:Residues: 1,'D',3,'EGKQ',8-16 <OSB>
C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
C:Keywords: blood coagulation; liver; phosphoprotein; plasma
F:1-16/Product: fibrinopeptide A #status experimental <APT>
F:3/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

Query Match 78.5%; Score 51; DB 2; Length 28;
Best Local Similarity 75.0%; Pred. No. 0.016; Indels 1; Gaps 0;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 BSDLFLAEGGGVR 13
: : : : :
Db 5 EGFTIARGGGVR 16

RESULT 13
B29501
fibrinopeptide A - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000
C:Accession: E29501
R:Blombaek, B.; Blombaek, M.; Hann, C.
unpublished results, cited by Blombaek, B., and Blombaek, M., in Chemotaxonomy and Ser
A:Reference number: A29501
A:Accession: E29501
A:Molecule type: protein
A:Residues: 1-17 <BLO>
R:Blombaek, B.; Blombaek, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A:Title: Studies on fibrinopeptides from mammals.
A:Reference number: A03118
A:Contents: annotation; confirmation of species assignment
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 75.4%; Score 49; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.022; Indels 1; Gaps 0;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 BSDLFLAEGGGVR 13
: : : : :
Db 6 KGEFLAEGGGVR 17

RESULT 14
I29501
fibrinopeptide A - kangaroo
C:Species: Macropus sp. (kangaroo)
C>Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
C:Accession: I29501
R:Blombaek, B.; Blombaek, M.; Hann, C.

unpublished results, cited by Blombaek, B., and Blombaek, M., in Chemotaxonomy and Ser
A:Reference number: A29501
A:Accession: I29501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <BLO>
C:Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 73.8%; Score 48; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 0.029; Indels 2; Gaps 0;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 BSDLFLAEGGGVR 13
: : : : :
Db 4 EGFTIARGGGVR 15

RESULT 15
B29501
fibrinopeptide A - European moose
C:Species: Alces alces alces (European moose, elk)
C>Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000
C:Accession: B29501
R:Blombaek, B.; Blombaek, M.; Hann, C.
unpublished results, cited by Blombaek, B., and Blombaek, M., in Chemotaxonomy and Ser
A:Reference number: A29501
A:Accession: B29501
A:Molecule type: protein
A:Residues: 1-19 <BLO>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 73.8%; Score 48; DB 2; Length 19;
Best Local Similarity 90.0%; Pred. No. 0.037; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DFLAEGGGVR 13
: : : : :
Db 10 EFLAEGGGVR 19

Search completed: February 10, 2003, 16:07:25
Job time : 18 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 10, 2003, 15:57:26 ; Search time 11 Seconds
(without alignments)
49.017 Million cell updates/sec

Title: US-09-845-729-1

Perfect score: 65

Sequence: 1 SESDFLAGGGVR 13

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	87.7	16	1 FIBA_MACFU	P12803 macaca fusc
2	57	87.7	19	1 FIBA_CEREL	P14446 cervus elap
3	57	87.7	866	1 FIBA_HUMAN	P02671 homo sapien
4	56	86.2	16	1 FIBA_CERSI	P14535 ceratotheri
5	54	83.1	16	1 FIBA_TAPTE	P14536 tapirus ter
6	53	81.5	16	1 FIBA_HYLLA	P14453 hyllobates l
7	53	81.5	18	1 FIBA_CAMDR	P14444 camelus dro
8	53	81.5	19	1 FIBA_EIBSO	P14441 bison bonas
9	53	81.5	19	1 FIBA_CERNI	P14447 cervus nipp
10	51	78.5	16	1 FIBA_FELCA	P14450 felis silve
11	51	78.5	28	1 FIBA_CANFA	P02673 canis famil
12	49	75.4	17	1 FIBA_PIG	P14460 sus scrofa
13	49	75.4	17	1 FIBA_LAMGL	P14454 lama glama
14	48	73.8	15	1 FIBA_SYNCA	P14463 syncerus ca
15	48	73.8	16	1 FIBA_EQUAS	P14449 equus asinu
16	48	73.8	16	1 FIBA_MANLE	P14455 mandrillus
17	48	73.8	16	1 FIBA_ODOHE	P14459 odocoileus
18	48	73.8	19	1 FIBA_BUBBU	P14442 bubalus bub
19	48	73.8	19	1 FIBA_SHEEP	P14451 ovis aries
20	48	73.8	596	1 FIBA_BOVIN	P02672 bos taurus
21	47	72.3	14	1 FIBA_HORSE	P14452 equus cabal
22	45	69.2	19	1 FIBA_MUNMU	P14457 muntiacus m
23	40	61.5	15	1 FIBA_ANAPL	P12801 anas platyr
24	40	61.5	1696	1 PCK5_BRACL	Q9nj15 branchiosto
25	39	60.0	13	1 FIBA_CAVPO	P14445 cavia porce
26	39	60.0	236	1 IPT_ERWHE	Q47851 erwina her
27	39	60.0	271	1 AAC3_PSEAE	P29808 pseudomonas
28	38	58.5	611	1 IF4B_HUMAN	P23588 homo sapien
29	38	58.5	742	1 SUN2_HUMAN	Q9uh99 homo sapien
30	37	56.9	19	1 FIBA_RANTA	P14462 rangifer ta
31	37	56.9	413	1 IDHC_SOYEN	Q06197 glycine max
32	37	56.9	415	1 IDHC_TOBAC	P50218 nicotiana t
33	37	56.9	416	1 IDHC_SOLTU	P50217 solanum tub

RESULT 1

FIBA_MACFU	ID	FIBA_MACFU	STANDARD;	PRT;	16 AA.
AC	P12803;				
DT	01-OCT-1989	(Rel. 12, Created)			
DT	01-OCT-1989	(Rel. 12, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).				
GN	FGA.				
OS	Macaca fuscata fuscata	(Japanese macaque),			P42084 bacillus su
OS	Macaca fascicularis	(Crab eating macaque) (Cynomolgus monkey),			P58080 streptococc
OS	Macaca mulatta	(Rhesus macaque)			Q40345 medicago sa
OS	Cercopithecus aethiops	(Green monkey) (Gorilla),			P14458 mustela vis
OS	Erythrocebus patas	(Red guenon) (Hussar),			P28320 saccharomyc
OS	Papio anubis	(Olive baboon),			Q9rz05 deinococcus
OS	Papio hamadryas	(Hamadryas baboon), and			Q9rh6 halobacteri
OS	Theropithecus gelada	(Gelada baboon).			Q35385 mus musculu
OC	Eukaryota;	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			P47256 mycoplasma
OC	Mammalia;	Eutheria; Primates; Catarrhini; Cercopitheidae;			P46340 bacillus su
OC	Cercopitheidae;	Macaca.			
OX	NCBI_TaxID=9543,	9541, 9544, 9534, 9538, 9555, 9557, 9565;			
RN	[1]				
RP	SEQUENCE.				
RC	SPECIES=E. patas, and M. fuscata;				
RX	MEDLINE=85289140; PubMed=3928610;				
RA	Nakamura S., Takenaka O., Takahashi K.;				
RT	"Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and				
RT	patas monkey (Erythrocebus patas): their amino acid sequences,				
RT	restricted mutations, and a molecular phylogeny for macaques,				
RT	quenons, and baboons."				
RL	J. Biochem. 97:1487-1492(1985).				
RN	[2]				
RP	SEQUENCE.				
RC	SPECIES=P. anubis, P. hamadryas, and T. gelada;				
RX	MEDLINE=84161822; PubMed=6423621;				
RA	Nakamura S., Takenaka O., Takahashi K.;				
RT	"Fibrinopeptides A and B of baboons (Papio anubis, papio hamadryas,				
RT	and Theropithecus gelada): their amino acid sequences and				
RT	evolutionary rates and a molecular phylogeny for the baboons."				
RL	J. Biochem. 94:1973-1978(1983).				
RN	[3]				
RP	SEQUENCE.				
RC	SPECIES=C. aethiops, M. mulatta, and M. fascicularis;				
RX	Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;				
RA	"Studies on fibrinopeptides from primates."				
RT	Acta Chem. Scand. 19:1788-1789(1965).				
CC	-1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT				
CC	POLYMERIZE INTO FIBRIN AND ACTING AS A COPOLYMER IN PLATELET				
CC	AGGREGATION.				
CC	-1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS				
CC	(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.				
CC	-1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY				
CC	THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA				
CC	CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES				
CC	RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.				
DR	PIR; A24180; A24180.				

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DR PIR; B24180; B24180.
DR PIR; A28854; A28854.
DR PIR; B28854; B28854.
DR PIR; C28854; C28854.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1551 MW; 49E8CBB63EA04DD3 CRC64;

Query Match 87.7%; Score 57; DB 1; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00034;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
: |||||
Db 5 EGDFLAEGGGVR 16

RESULT 2
FIBA CEREL STANDARD; PRT; 19 AA.
AC P1446;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Cervus elaphus (Red deer), and
OS Cervus elaphus nelsoni (American elk).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860, 9864;
RN [1]
RP SEQUENCE.
RC SPECIES=C.elaphus;
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
RN [2]
RP SEQUENCE.
RC SPECIES=C.e.nelsoni;
RA Moss G.A., Doolittle R.F.;
RT "Amino acid sequence studies on artiodactyl fibrinopeptides.";
RL Arch. Biochem. Biophys. 122:674-684(1967).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 19 FIBRINOPEPTIDE A.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 1808 MW; 9BA54C26873B59C5 CRC64;

Query Match 87.7%; Score 57; DB 1; Length 19;
Best Local Similarity 84.6%; Pred. No. 0.00041;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SSDFLAEGGGVR 13
: |||||
Db 7 ASSDFLAEGGGVR 19

RESULT 3
FIBA HUMAN STANDARD; PRT; 866 AA.
ID FIBA_HUMAN
AC P02671; Q9BX62; Q9UCH2;
DT. 21-JUL-1986 (Rel. 01, Created)

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DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha/alpha-E chain precursor [Contains: Fibrinopeptide A].
GN FGA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ALPHA-E FORM).
RX MEDLINE=93090725; PubMed=1457396;
RA Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,
RA Roy S.N., Redman C.M., Grieninger G.;
RT "Carboxy-terminal-extended variant of the human fibrinogen alpha
RT subunit: a novel exon conferring marked homology to beta and gamma
RT subunits.";
RL Biochemistry 31:11968-11972(1992).
RN [2]
RP SEQUENCE FROM N.A. (ALPHA-E FORM).
RX Chung D.W., Grieninger G.;
RT "Fibrinogen DNA and protein sequences.";
RL (In) Ebert R.F. (eds.);
RL Index of variant human fibrinogens, pp.13-24, CRC Press,
RL Boca Raton (1994).
RN [3]
RP SEQUENCE FROM N.A. (ALPHA-E; ALPHA), AND VARIANTS VAL-6; ALA-331 AND
RP ALA-456.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Pool C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-655 FROM N.A. (ALPHA-E FORM).
RC TISSUE=Liver;
RX MEDLINE=91344740; PubMed=2102623;
RA Chung D.W., Harris J.B., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
RT fibrinogen.";
RL Adv. Exp. Med. Biol. 281:39-48(1990).
RN [5]
RP SEQUENCE FROM N.A. (ALPHA FORM).
RX MEDLINE=83247396; PubMed=6575389;
RA Kant J.A., Lord S.T., Crabtree G.R.;
RT "Partial mRNA sequences for human A alpha, B beta, and gamma
RT fibrinogen chains: evolutionary and functional implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957(1983).
RN [6]
RP SEQUENCE OF 1-629 FROM N.A.
RX MEDLINE=83283432; PubMed=6688355;
RA Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RT the alpha chain of human fibrinogen.";
RL Biochemistry 22:3237-3244(1983).
RN [7]
RP SEQUENCE OF 20-629.
RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
RT structural variants.";
RL (In) Peeters H. (eds.);
RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
RL Pergamon Press, Oxford (1980).
RN [8]
RP SEQUENCE OF 20-629, AND DISULFIDE BONDS.
RX MEDLINE=80088231; PubMed=518846;
RA Watt K.W.K., Cottrell B.A., Strong D.D., Doolittle R.F.;
RT "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT Overlapping sequences providing the complete sequence.";
RL Biochemistry 18:5410-5416(1979).
RN [9]
RP SEQUENCE OF 110-156 FROM N.A.
RX MEDLINE=84069777; PubMed=6689067;
RA Imam A.M., Eaton M.A., Williamson R., Humphries S.;
RT "Isolation and characterisation of cDNA clones for the A alpha- and
RT gamma-chains of human fibrinogen.";

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OX NCBI_TaxID=9807;
RN [1]
RP SEQUENCE.
RA O'Neil P.B., Doolittle R.F.;
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL Syst. Zool. 22:590-595(1973).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1639 MW; 0958CBB6293F4C81 CRC64;

Query Match 86.2%; Score 56; DB 1; Length 16;
Best Local Similarity 76.9%; Pred. No. 0.00052;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SESDFLAEGGVR 13
Db 4 TEGDFTAEAGGVR 16
:|:|||||

RESULT 5
FIBA_TAPTE STANDARD; PRT; 16 AA.
AC P14536;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Tapirus terrestris (Lowland tapir) (Brazilian tapir).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX NCBI_TaxID=9801;
RN [1]
RP SEQUENCE.
RA O'Neil P.B., Doolittle R.F.;
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL Syst. Zool. 22:590-595(1973).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1622 MW; 48598EB6292F4030 CRC64;

Query Match 83.1%; Score 54; DB 1; Length 16;
Best Local Similarity 76.9%; Pred. No. 0.0012;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SESDFLAEGGVR 13
Db 4 TEGEFLAEGGVR 16
:|:|||||

RESULT 6
FIBA_HYLLA STANDARD; PRT; 16 AA.
ID FIBA_HYLLA

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AC P14453;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Hylobates lar (Common gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9580;
RN [1]
RP SEQUENCE.
RA MEDLINE=70294424; PubMed=5466708;
RA Gross G.A., Doolittle R.F., Roberts B.F.;
RT "Gibbon fibrinopeptides: identification of a glycine-serine allelism
RT at position B-3.";
RL Science 170:468-470(1970).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1565 MW; 49E98EB63EA04DD3 CRC64;

Query Match 81.5%; Score 53; DB 1; Length 16;
Best Local Similarity 83.3%; Pred. No. 0.0018;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGVR 13
Db 5 EGEFLAEGGVR 16
:|:|||||

RESULT 7
FIBA_CAMDR STANDARD; PRT; 18 AA.
ID FIBA_CAMDR
AC P1444;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Camelus dromedarius (Dromedary) (Arabian camel).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838;
RN [1]
RP SEQUENCE.
RA MEDLINE=67209145; PubMed=6033721;
RA Doolittle R.F., Schubert D., Schwartz S.A.;
RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT Dromedary camel, mule deer, and cape buffalo.";
RL Arch. Biochem. Biophys. 118:456-467(1967).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 18 FIBRINOPEPTIDE A.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1835 MW; 244448763D7F4CC6 CRC64;

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Query Match      81.5%; Score 53; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.002;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
   : |||||
Db 7 EGDFLAEGGGVR 18
   : |||||

RESULT 8
FIBA_BISBO
ID_FIBA_BISBO STANDARD; PRT; 19 AA.
AC P1441;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Bison bonasus (European bison).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bison.
OX NCBI_TaxID=9902;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC Blood coagulation; Plasma.
KW PEPTIDE 1 19 FIBRINOPEPTIDE A.
FT NON TER 19
FT SEQUENCE 19 AA; 1836 MW; 9BA55A0F473B59C5 CRC64;

Query Match      81.5%; Score 53; DB 1; Length 19;
Best Local Similarity 76.9%; Pred. No. 0.0021;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SESDFLAEGGGVR 13
   : |||||
Db 7 ASGDFLAEGGGVR 19
   : |||||

RESULT 9
FIBA_CERNI
ID_FIBA_CERNI STANDARD; PRT; 19 AA.
AC P1447;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Cervus nippon (Sika deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9863;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J., Holmberg E.;
RT "Structure of fibrinopeptides-its relation to enzyme specificity and
RT phylogeny and classification of species.";
RL Ark. Remi 25:411-428(1966).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT

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CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC Blood coagulation; Plasma.
KW NON TER 19
KW SEQUENCE 19 AA; 1822 MW; 9BA40926873B59C5 CRC64;

Query Match      81.5%; Score 53; DB 1; Length 19;
Best Local Similarity 76.9%; Pred. No. 0.0021;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SESDFLAEGGGVR 13
   : |||||
Db 7 ASSEFLAEGGGVR 19
   : |||||

RESULT 10
FIBA_FELCA
ID_FIBA_FELCA STANDARD; PRT; 16 AA.
AC P14450;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC Blood coagulation; Plasma.
KW PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON TER 16
FT SEQUENCE 16 AA; 1620 MW; C3C98EB62D6CC7D3 CRC64;

Query Match      78.5%; Score 51; DB 1; Length 16;
Best Local Similarity 75.0%; Pred. No. 0.004;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
   : |||||
Db 5 EGDFLAEGGGVR 16
   : |||||

RESULT 11
FIBA_CANFA
ID_FIBA_CANFA STANDARD; PRT; 28 AA.
AC P02673; P14464;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Canis familiaris (Dog), and
OS Vulpes vulpes (Red fox).

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CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615, 9627;
RN [1]
RP SEQUENCE.
RC SPECIES=C.familiaris;
RX MEDLINE=76081726; PubMed=1198547;
RA Birken S., Wilner G.D., Canfield R.E.;
RT "Studies of the structure of canine fibrinogen.";
RL Thromb. Res. 7:599-610(1975).
RN [2]
RP SEQUENCE OF 1-16.
RC SPECIES=C.familiaris, and V.vulpes;
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides A and B from alpha & beta
RL Acta Chem. Scand. 19:1789-1791(1965).
RN [3]
RP SEQUENCE OF 1-16.
RC SPECIES=C.familiaris;
RX MEDLINE=66020594; PubMed=5836555;
RA Osbahr A.J. Jr., Colman R.W., Laki K., Gladner J.A.;
RT "The nature of the peptides released from canine fibrinogen.";
RL Biochem. Biophys. Res. Commun. 14:555-558(1964).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; A03118; A03118.
DR PIR; A05296; A05296.
KW Blood coagulation; Plasma; Phosphorylation.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT MOD RES 3 3 PHOSPHORYLATION (IN SOME MOLECULES).
FT CONFLICT 2 2 N -> D (IN REF. 2).
FT CONFLICT 4 7 KESE -> EGKQ (IN REF. 2).
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 2958 MW; 09DCD3F923BFEBD2 CRC64;

Query Match 78.5%; Score 51; DB 1; Length 28;
Best Local Similarity 75.0%; Pred. No. 0.0072;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
DB 5 EGEFLAEGGGVR 16
| : : : : :
| : : : : :

RESULT 12
FIBA_PIG
ID FIBA_PIG STANDARD; PRT; 17 AA.
AC P14460;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS

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CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1762 MW; 232EFEB8B86B0A0C CRC64;

Query Match 75.4%; Score 49; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.0098;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
DB 6 KGEFLAEGGGVR 17
| : : : : :
| : : : : :

RESULT 13
FIBA_LAMGL
ID FIBA_LAMGL STANDARD; PRT; 18 AA.
AC P14454;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Lama glama (Llama), and
OS Lama vicugna (Vicugna)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=9844, 9843;
RN [1]
RP SEQUENCE.
RC SPECIES=L.vicugna;
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
RN [2]
RP SEQUENCE.
RC SPECIES=L.vicugna;
RA Moss G.A., Doolittle R.F.;
RT "Amino acid sequence studies on artiodactyl fibrinopeptides.";
RL Arch. Biochem. Biophys. 122:674-684(1967).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 18 FIBRINOPEPTIDE A.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1834 MW; 2444487B8B7F4CC6 CRC64;

Query Match 75.4%; Score 49; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 0.01;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGGVR 13
DB 7 KGEFLAEGGGVR 18
| : : : : :
| : : : : :

RESULT 14
FIBA_SYNCA
ID FIBA_SYNCA STANDARD; PRT; 15 AA.
AC P14463;
DT 01-JAN-1990 (Rel. 13, Created)

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01-JAN-1990 (Rel. 13, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Syncerus caffer (Cape buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Syncerus.
 OX NCBI_TaxID=9970;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=67209145; PubMed=6033721;
 RA Doolittle R.F., Schubert D., Schwartz S.A.;
 RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
 RT Dromedary camel, mule deer, and cape buffalo."
 RL Arch. Biochem. Biophys. 118:456-467(1967).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 15 FIBRINOPEPTIDE A.
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1480 MW; 4E998EA5F0B41CC6 CRC64;

 Query Match 73.8%; Score 48; DB 1; Length 15;
 Best Local Similarity 90.0%; Pred. No. 0.013;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 4 DFLAEGGGVR 13
 :|||||||
 DB 6 EFLAEGGGVR 15

 RESULT 15
 FIBA EQUAS STANDARD; PRT; 16 AA.
 ID P14449;
 AC 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Equus asinus (Donkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9793;
 RN [1]
 RP SEQUENCE.
 RX Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals."
 RL Acta Chem. Scand. 19:1789-1791(1965).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
 FT NON TER 16 16
 SQ SEQUENCE 16 AA; 1696 MW; 09598EB63C2A5957 CRC64;

 Query Match 73.8%; Score 48; DB 1; Length 16;
 Best Local Similarity 66.7%; Pred. No. 0.014;

Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ESDFLAEGGGVR 13
 :||:|||||
 DB 5 EGEFISEGGGVR 16

 Search completed: February 10, 2003, 16:01:06
 Job time : 12 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 10, 2003, 15:57:51 ; Search time 92 Seconds
(without alignments)
29.115 Million cell updates/sec

Title: US-09-845-729-1

Perfect score: 65

Sequence: 1 SESDFLAEGGGVR 13

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	57	87.7	218	4 Q8WW76	Q8ww76 homo sapien
2	46	70.8	557	11 Q99K47	Q99k47 mus musculus
3	43	66.2	260	10 Q8S2N9	Q8s2n9 oryza sativ
4	41	63.1	242	5 Q8T925	Q8t925 tetrahymena
5	41	63.1	552	2 Q9APX1	Q9apx1 pseudomonas
6	40	61.5	280	16 Q99WM6	Q99wm6 staphylococ
7	40	61.5	630	13 Q8UW15	Q8uw15 lapemis har
8	40	61.5	852	5 Q9U4G5	Q9u4g5 drosophila
9	39	60.0	89	16 Q98F73	Q98f73 rhizobium l
10	39	60.0	171	3 Q9P8L5	Q9p8l5 botrytis ci
11	39	60.0	186	2 Q9F7D5	Q9f7d5 salmonella
12	39	60.0	245	16 Q8Z6K4	Q8z6k4 salmonella
13	39	60.0	245	16 Q9Z4S4	Q9z4s4 salmonella
14	39	60.0	324	16 Q53481	Q53481 mycobacteri
15	39	60.0	465	10 Q9LH81	Q9lh81 arabidopsis
16	39	60.0	465	10 Q940V4	Q940v4 arabidopsis

17	39	60.0	481	10 Q8W0R4	Q8w0r4 sorghum bic
18	39	60.0	546	5 Q9VHD0	Q9vhd0 drosophila
19	39	60.0	705	2 Q85866	Q85866 sphingomona
20	39	60.0	748	10 Q8W0N1	Q8w0n1 oryza sativ
21	39	60.0	753	10 Q9LIC9	Q9lic9 arabidopsis
22	39	60.0	1159	4 Q9NV34	Q9nv34 homo sapien
23	39	60.0	1165	4 Q9NZQ8	Q9nzq8 homo sapien
24	38.5	59.2	741	16 Q8UR11	Q8ur11 agrobacteri
25	38	58.5	99	16 Q8ZQ92	Q8zq92 salmonella
26	38	58.5	147	10 Q9MAV0	Q9mav0 arabidopsis
27	38	58.5	256	16 Q92LM7	Q92lm7 rhizobium m
28	38	58.5	440	4 Q9UH99	Q9uh99 homo sapien
29	38	58.5	575	10 Q9LZM8	Q9lzm8 arabidopsis
30	38	58.5	611	4 Q8WYK5	Q8wyk5 homo sapien
31	38	58.5	652	16 Q8YFV7	Q8yfpv7 anabaena sp
32	38	58.5	669	17 Q9YFF9	Q9yff9 aeropyrum p
33	38	58.5	686	10 Q9T0B3	Q9t0b3 arabidopsis
34	38	58.5	722	10 Q8VYR4	Q8vyr4 arabidopsis
35	38	58.5	727	10 Q9T0B4	Q9t0b4 arabidopsis
36	38	58.5	730	10 Q22989	Q22989 arabidopsis
37	38	58.5	742	4 Q75156	Q75156 homo sapien
38	38	58.5	770	10 Q22988	Q22988 arabidopsis
39	38	58.5	1458	12 Q8QTB8	Q8qtb8 white spot
40	38	58.5	2330	12 Q91L86	Q91l86 white spot
41	38	58.5	4180	12 Q8VAQ8	Q8vaq8 white spot
42	37	56.9	79	10 Q8RUJ7	Q8ruj7 helianthus
43	37	56.9	127	3 Q9HGG0	Q9hgg0 cryptococcus
44	37	56.9	127	3 Q9HGF9	Q9hgf9 cryptococcus
45	37	56.9	135	3 Q9HGG3	Q9hgg3 cryptococcus

ALIGNMENTS

RESULT 1

Q8WW76 PRELIMINARY; PRT; 218 AA.

AC Q1-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Similar to fibrinogen, A alpha polypeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020764; AAH20764.1; -
SQ SEQUENCE 218 AA; 24695 MW; 36D756A8116EA94A CRC64;

Query Match 87.7%; Score 57; DB 4; Length 218;
Best Local Similarity 91.7%; Pred. No. 0.033;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 24 EGDFLAEGGGVR 35

RESULT 2

Q99K47 PRELIMINARY; PRT; 557 AA.

AC Q99K47;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Fibrinogen A alpha polypeptide.
GN FGA.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005467; AAH05467.1; -.
DR HSP; P02671; 1FZA.
DR MGD; MGI:1316726; Fga.
SQ SEQUENCE 557 AA; 61325 MW; C47F496D1BA432DE CRC64;

Query Match 70.8%; Score 46; DB 11; Length 557;
Best Local Similarity 66.7%; Pred. No. 8.4;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ESDFLAEGGVR 13
: : : : :
Db 25 KGEFLSEGGVR 36

RESULT 3

Q8S2N9 ID Q8S2N9 PRELIMINARY; PRT; 260 AA.

AC Q8S2N9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE B1066G12.16 protein.
GN B1066G12.16.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]

RP SEQUENCE FROM N.A.
RA STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC clone: B1066G12.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003201; BAB89442.1; -.
SQ SEQUENCE 260 AA; 29524 MW; 40929C6C486F0F06 CRC64;

Query Match 66.2%; Score 43; DB 10; Length 260;
Best Local Similarity 69.2%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SESDFLAEGGVR 13
: : : : :
Db 188 SESDPVAGSGLR 200

RESULT 4

Q8T925 ID Q8T925 PRELIMINARY; PRT; 242 AA.

AC Q8T925;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Igr2p.
GN IGR2.
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymena.
OX NCBI_TaxID=5911;
RN [1]_TaxID=5911;

RP SEQUENCE FROM N.A.
RA Turkewitz A.P., Haddad A.;
RT "A non-architectural cargo protein in Tetrahymena thermophila dense core secretory granules.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY075152; AAL79515.1; -.
SQ SEQUENCE 242 AA; 27000 MW; A1E687237B618E8A CRC64;

Query Match 63.1%; Score 41; DB 5; Length 242;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SESDFLAEGG 10
: : : : :
Db 77 SKNDFIAEGG 86

RESULT 5

Q9APX1 ID Q9APX1 PRELIMINARY; PRT; 552 AA.

AC Q9APX1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative amino acid transport protein.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]

RP SEQUENCE FROM N.A.
RA MEDLINE=21142509; PubMed=11208781;
RA Liang X., Pham X.Q.T., Olson M.V., Lory S.;
RT "Identification of a Genomic Island Present in the Majority of Pathogenic Isolates of Pseudomonas aeruginosa.";
RL J. Bacteriol. 183:843-853(2001).

DR EMBL; AF241171; AAK01502.1; -.
DR InterPro; IPR001734; Na/solut_sympot.
DR Pfam; PF00474; SSP; 1.
DR TIGRFAMs; TIGR00813; sss; 1.
DR PROSITE; PS00456; NA_SOLUT_SYMP_1; UNKNOWN_1.
DR PROSITE; PS0283; NA_SOLUT_SYMP_3; 1.
SQ SEQUENCE 552 AA; 58956 MW; 7A45F15BC8065C09 CRC64;

Query Match 63.1%; Score 41; DB 2; Length 552;
Best Local Similarity 53.8%; Pred. No. 65;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SESDFLAEGGVR 13
: : : : :
Db 58 STADFYSAGGIR 70

RESULT 6

Q99WM6 ID Q99WM6 PRELIMINARY; PRT; 280 AA.

AC Q99WM6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein SAV0351.
GN SAV0351 OR SA0339.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Karamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mitsuhashi Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Hiramatsu K.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein ms13900.
 GN MSL3900.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 NCBI_TaxID=381;
 [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003003; BAB50694.1; -;
 KW Hypothetical protein, Complete proteome.
 SQ SEQUENCE 89 AA; 10058 MW; 5197B7CB06AFC351 CRC64;
 Query Match 60.0%; Score 39; DB 16; Length 89;
 Best Local Similarity 61.5%; Pred. No. 20;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 SESDFLAEGGGV 13
 |||:|:|:|:|:
 Db 25 SEVEFVATDGGVR 37

RESULT 10
 Q9P8L5 PRELIMINARY; PRT; 171 AA.
 ID Q9P8L5
 AC Q9P8L5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE ABC transporter-like protein (Fragment).
 GN BCATRJ.
 OS Botrytis cinerea (Botryotinia fuckeliana).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
 OC Helotiales; Sclerotiniaceae; Botryotinia.
 NCBI_TaxID=40559;
 [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=B05.10;
 RA Schoonbeek H., Vermeulen T., Hayashi K., De Waard M.A.;
 RT "Differential expression of membrane-bound transporters in Botrytis
 RT cinerea.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF238228; AAF64438.1; -;
 DR InterPro; IPR004147; ABC1.
 DR Pfam; PF03109; ABC1; 1.
 DR NON_TER 1
 FT NON_TER 171 171
 SQ SEQUENCE 171 AA; 19561 MW; 15515C19C9FBB1F9 CRC64;
 Query Match 60.0%; Score 39; DB 3; Length 171;
 Best Local Similarity 70.0%; Pred. No. 41;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 SDFLAEGGGV 12
 |||:|:|:|:|:
 Db 159 SDFMENGGV 168

RESULT 11
 Q9F7D5 PRELIMINARY; PRT; 186 AA.
 ID Q9F7D5
 AC Q9F7D5;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 20.7 kDa protein (Fragment).
 GN NIT.
 OS Salmonella enterica subsp. enterica serovar Typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 NCBI_TaxID=90371;
 [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RX MEDLINE=21172862; PubMed=11274105;
 RA Price-Carter M., Tingey J., Bobik T.A., Roth J.R.;
 RT "The Alternative Electron Acceptor Tetrathionate Supports B12-
 RT Dependent Anaerobic Growth of Salmonella enterica Serovar Typhimurium
 RT on Ethanolamine or 1,2-Propanediol.";
 RL J. Bacteriol. 183:2463-2475(2001).
 DR EMBL; AF282268; AAG31761.1; -;
 KW Hypothetical protein.
 FT NON_TER 186 186
 SQ SEQUENCE 186 AA; 20711 MW; 6B5FE0B04E07CFA0 CRC64;
 Query Match 60.0%; Score 39; DB 2; Length 186;
 Best Local Similarity 60.0%; Pred. No. 45;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SDFLAEGGGV 12
 |||:|:|:|:|:
 Db 102 ADYVAEGGGL 111

RESULT 12
 Q8Z6K4 PRELIMINARY; PRT; 245 AA.
 ID Q8Z6K4
 AC Q8Z6K4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Orf 245 protein.
 GN STY1741.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 NCBI_TaxID=601;
 [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Conerton P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 DR EMBL; AL627271; CAD01984.1; -;
 DR InterPro; IPR003006; IG_MHC.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 245 AA; 27429 MW; 11BF3BA03D62E3E3 CRC64;
 Query Match 60.0%; Score 39; DB 16; Length 245;
 Best Local Similarity 60.0%; Pred. No. 61;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SDFLAEGGGV 12
 |||:|:|:|:|:
 Db 102 ADYVAEGGGL 111

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RESULT 13
Q92454
ID Q92454 PRELIMINARY; PRT; 245 AA.
AC
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE ORF 245 protein (Putative cytoplasmic protein).
OS ORF245 OR STM1381.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
NCBI_TaxID=602;
RN (1)
RP SEQUENCE FROM N.A.
RC
RC STRAIN=LT2;
RC MEDLINE=99157556; PubMed=10027966;
RX Hensel M., Egeiseer C., Nikolaus T.;
RX "Molecular and functional analysis indicates a mosaic structure of
RT Salmonella Pathogenicity Island 2.";
RT Mol. Microbiol. 31:489-498(1999).
RN (2)
RP SEQUENCE FROM N.A.
RC
RC STRAIN=LT2;
RC Hensel M., Hinsley A.P., Nikolaus T., Savers G., Berks B.C.;
RX "he genetic basis of tetrathionate respiration in Salmonella
RT typhimurium.";
RT Mol. Microbiol. 0:0-0(0).
RN (3)
RP SEQUENCE FROM N.A.
RC
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RC MEDLINE=21534948; PubMed=11677609;
RX McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RA Nature 413:852-856(2001).
RRL Nature 413:852-856(2001).
DR EMBL; AJ224978; CAB37418.1; -
DR EMBL; AB008760; AAL20305.1; -
DR InterPro; IPR003006; IG_MHC.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 245 AA; 27430 MW; FFBF31AA9DC8E943 CRC64;

Query Match 60.8%; Score 39; DB 16; Length 245;
Best Local Similarity 60.8%; Pred. No. 61;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 SDFLAEGGGV 12
:|::|::|::|
DB 102 ADYVAEGGGL 111

RESULT 14
Q53481
ID Q53481 PRELIMINARY; PRT; 324 AA.
AC
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative transmembrane protein.
DE RV2037C OR MT2097 OR MTV018.24C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
RN (1)
RP SEQUENCE FROM N.A.

```

DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00096; CYTOCHROME P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 465 AA; 53862 MW; 630A21D0765E0D0D CRC64;

```
Query Match      60.0%; Score 39; DB 10; Length 465;
Best Local Similarity 69.2%; Pred. NO. 1.2e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 SESDFLAEGGVR 13
| : | | | | |
Db 401 SKSYFLLFCGGVR 413

Search completed: February 10, 2003, 16:02:46
Job time : 95 secs